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FIGURE 88

MAAASRSASGWALLLLVALWQQRAAGSGVFQLQLQEFINERGVLASGRPCEPGCRTFFFRVCLK
HFQAVVSPGPCTFGTVSTPVLGTNSFAVRDDSSGGGRNPLQLPFNFTWPGTFSLIIEAWHAPG
DDLRLPEALPPDALISKIAIQGSLAVGQNWLLDEQTSTLTRLRYSYRVICSDNYYGDNCSRLCK
KRNDHFGHYVCQPDGNLSCLPGWTGEYCQQPICLSGCHEQNGYCSKPAECLCRPGWQGRLCNE
CIPHNGCRHGTCSTPWQCTCDEGWGGLFCDQDLNYCTHHS PCKNGATCSNSGQRSYTCTCRPG
YTGVDCELELSECDSNPCRNGGSKDQEDGYHCLCPPGYGLHCEHSTLSCADSPCFNGGSCR
ERNQGANYACECPPNFTGSNCEKKVDRCTSNPCANGGQCLNRGPSRMCRCPGFTGT YCELHV
SDCARNPCAHHGTCHDLNGLMCTCPAGFSGRRCEVRTSIDACASSPCFN RATCYTDLSTDTF
VCNCPYGFVGSRCFFVGLPPSF PWVAVSLGVGLAVLLVLLGMVAVAVRQLRLRRPDDGSREA
MNNLSDFQKDNLI PAAQLKNTNQKKELEVDCGLDKSNCGKQQNHTLDYNLAPGPLGRGTMPGK
FPHSDKSLGEKAPLRLHSEKPECRISAICSPRDSMYQSVCLISEERNECVIATEV

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 530-552

N-glycosylation sites.

amino acids 108-112, 183-187, 205-209, 393-397, 570-574, 610-614

Glycosaminoglycan attachment site.

amino acids 96-100

Tyrosine kinase phosphorylation site.

amino acids 340-347

N-myristoylation sites.amino acids 42-48, 204-210, 258-264, 277-283, 297-303, 383-389,
415-421, 461-467, 522-528, 535-541, 563-569, 599-605, 625-631**Amidation site.**

amino acids 471-475

Aspartic acid and asparagine hydroxylation site.

amino acids 339-351

EGF-like domain cysteine pattern signature.amino acids 173-185, 206-218, 239-251, 270-282, 310-322, 348-360,
388-400, 426-438, 464-476, 506-518**Calcium-binding EGF-like:**amino acids 224-245, 255-276, 295-316, 333-354, 373-394, 411-432,
449-470

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FIGURE 89

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGAC
TTGACTCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGC
CGCCCAGTCCCGGCCCCCTCTCCCGCCCCACACCCACCCTCCTGGCTCTTCCTGTTTTTACTCC
TCCTTTTCATTTCATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCAAGCC
GAGCGTGGAAGAATCGGGTTCCTCGGGACCGGCACTTGGAATTCTGGTGTTAGTGCTCCCGATT
CAAGCTTTCCCCAAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCA
GAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAAAAAACATATCCT
CCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTTGTTGATAACTTGAACCTGCTAAAGGCA
ATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCACTTGATAAT
AAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGATTATGACTCT
ACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATCAACTAGACGGG
ACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAGAAAATGAC
AGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGCCAA
GCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAAATTAATCTCAAAGGAAGCCAAC
AATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCA
GAGAAAGTGAATCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACA
GTATCTAACACATTAACCTTGACAAATGGCTTGGAAGGAGAACTAAAACCTACAGTGAAGAC
AACTTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTCAGAA
AAAGAAGCAAAGAGAGAAAGAAACACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAG
ATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTTCCTACCTTGAAAACCTGGAT
GAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAATGCTACTGACAATATAAGCAAG
CTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGACAGTACCAAGGAAGAAGCAGCT
AAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAAGATGATAACTCCAACCCAGGA
GGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGCCATCAGAAAAAATATT
GAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGAAGATTATGACCTTTCAAAGATGAGA
GACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAAGAAGCC
GAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAATGGCAAAAGATCCAGGAGTCTTTC AAC
TGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAAATTTTTTGACCC
AAGGGTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGC
TTTCTTCCCGTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAATAAAAAAAAAA
AAA

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FIGURE 90

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENK
PGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSG
LDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTL
EDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTFMAAIQDGLAKGENDETVSNT
LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVK
YGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPAPEKSHEETDSTKEEAAKMEK
EYGLKDDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDL SKMRDFIN
KQADAYVEKGILDKEEA EAIKRIYSSL

Important features:**N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

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FIGURE 91

TGCATCAGTGCCCAGGCAAGCCCAGGAGTTGACATTTCTCTGCCCAGCCATGGGCCTCACCCCT
GCTCTTGCTGCTGCTCCTGGGACTAGAAGGTCAGGGCATAGTTGGCAGCCTCCCTGAGGTGCT
GCAGGCACCCGTGGGAAGCTCCATTCTGGTGCAGTGCCACTACAGGCTCCAGGATGTCAAAGC
TCAGAAAGGTGTGGTGCCGGTTCTTGCCGGAGGGGTGCCAGCCCCTGGTGTCTCAGCTGTGGA
TCGCAGAGCTCCAGCGGGCAGGCGTACGTTTCTCACAGACCTGGGTGGGGGCCTGCTGCAGGT
GGAAATGGTTACCCTGCAGGAAGAGGATGCTGGCGAGTATGGCTGCATGGTGGATGGGGCCAG
GGGGCCCCAGATTTTGCACAGAGTCTCTCTGAACATACTGCCCCCAGAGGAAGAAGAAGAGAC
CCATAAGATTGGCAGTCTGGCTGAGAACGCATTCTCAGACCCTGCAGGCAGTGCCAACCCTTT
GGAACCCAGCCAGGATGAGAAGAGCATCCCCTTGATCTGGGGTGCTGTGCTCCTGGTAGGTCT
GCTGGTGGCAGCGGTGGTGTGTTTGTGTGATGGCCAAGAGGAACAAGAATCCCTCCTCAG
TGGTCCACCACGTCAAGTGACTCTGGACCGGCTGCTGAATTGCCTTTGGATGTACCACACATTA
GGCTTGACTCACCACTTCATTTGACAATACCACCTACACCAGCCTACCTCTTGATTCCCCAT
CAGGAAAACCTTCACTCCCAGCTCCATCCTCATTGCCCCCTCTACCTCCTAAGGTCCTGGTCT
GCTCCAAGCCTGTGACATATGCCACAGTAATCTTCCCGGGAGGGAACAAGGGTGGAGGGACCT
CGTGTGGGCCAGCCCAGAATCCACCTAACAATCAGACTCCATCCAGCTAAGCTGCTCATCACA
CTTTAAACTCATGAGGACCATCCCTAGGGGTTCTGTGCATCCATCCAGCCAGCTCATGCCCTA
GGATCCTTAGGATATCTGAGCAACCAGGGACTTTAAGATCTAATCCAATGTCCTAACTTTACT
AGGGAAAGTGACGCTCAGACATGACTGAGATGTCTTGGGGAAGACCTCCCTGCACCCAACTCC
CCCACTGGTTCTTCTACCATTACACACTGGGCTAAATAAACCCTAATAATGATGTGCAAAAAA
AAA

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FIGURE 92

MGLTLLLLLLLLGLEGQGIVGSLPEVLQAPVGSSILVQCHYRLQDVKAQKVWCRFLPEGCQPLV
SSAVDRRAPAGRRTFLTDLGGGLLQVEMVTLQEEDAGEYGCMVDGARGPQILHRVSLNILPPE
EEEETHKIGSLAENAFSDPAGSANPLEPSQDEKSIPLIWGAVLLVGLLVAAVVLFAVMAKRKQ
ESLLSGPPRQ

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 161-181

N-myristoylation sites.

amino acids 17-23, 172-178

Amidation site.

amino acids 73-79

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FIGURE 93

GGCGGCGTTGCCGGGCTCTCCGGAAGGAGACGTGGCGGCGGTTGGGCGGTTGATACCCGGGCG
CTTTATAGTCCCGCCGCCTCCTCCTCCACCTCCTCCTCCTCCTCCTCCTGCGGCGAGAG
GAGGTTGTGGCGGTGGCTGGAGAAAGCGGCGGCGGAGG**ATG**GAGGAAGGAGGCGGCGGCGGTAC
GGAGTCTGGTCCCGGGCGGGCCGGTGTACTGGTCCTCTGCGGCCTCCTGGAGGCGTCCGGCG
GCGGCCGAGCCCTTCCCTCAACTCAGCGATGACATCCCTTTCCGAGTCAACTGGCCCCGGCACCG
AGTTCTCTCTGCCACAACCTGGAGT¹TTTATATAAAGAAGATAATTATGTCATCATGACAACCTG
CACATAAAGAAAAATATAAATGCATACTTCCCCTTGTGACAAGTGGGGATGAGGAAGAAGAAA
AGGATTATAAAGGCCCTAATCCAAGAGAGCTTTTGGAGCCACTATTTAAACAAAGCAGTTGTT
CCTACAGAATTGAGTCTTATTGGACTTACGAAGTATGTCATGGAAAACACATTCGGCAGTACC
ATGAAGAGAAAGAACTGGTCAGAAAATAAATATTCACGAGTACTACCTTGGGAATATGTTGG
CCAAGAACCTTCTATTTGAAAAAGAACGAGAAGCAGAAGAAAAGGAAAAATCAAATGAGATTCT
CCACTAAAAATATCGAAGGTGAGATGACACCATACTATCCTGTGGGAATGGGAAATGGTACAC
CTTGTAGTTTGAACAGAACCGGCCAGATCAAGTACTGTGATGTACATATGTCATCCTGAAT
CTAAGCATGAAATTCTTTCAGTAGCTGAAGTTACAACCTTGTGAATATGAAGTTGTCATTTTGA
CACCCTCTTGTGCAGTCATCCTAAATATAGGTTTCAAGCATCTCCTGTGAATGACATATTTT
GTCAATCACTGCCAGGATCTCCATTTAAGCCCCTCACCTTGAGGCAGCTGGAGCAGCAGGAAG
AAATACTAAGGGTGCCTTTTAGGAGAAATAAAGAGGGTGTGCGTTGGTGGAAATATGAATTCT
GCTATGGCAAACATGTACATCAATACCATGAGGACAAGGATAGTGGGAAAACCTCTGTGGTTG
TCGGGACATGGAACCAAGAAGAGCATATTGAATGGGCTAAGAAGAATACTGCTAGAGCTTATC
ATCTTCAAGACGATGGTACCCAGACAGTCAGGATGGTGTACATTTTTTATGGAAATGGAGATA
TTTGTGATATAACTGACAAACCAAGACAGGTGACTGTAAAACATAAAGTGCAAAGAATCAGATT
CACCTCATGCTGTTACTGTATATATGCTAGAGCCTCACTCCTGTCAATATATTCTTGGGGTTG
AATCTCCAGTGATCTGTAAAATCTTAGATACAGCAGATGAAAATGGACTTCTTTCTCTCCCA
ACTAAAGGATATTAAAGTTAGGGGAAAGAAAAGATCATTGAAAGTCATGATAATTTCTGTCCC
ACTGTGTCTCATTATAGAGTTCTCAGCCATTGGACCTCTTCTAAAGGATGGTATAAAATGACT
CTCAACCCTTTGTGAATACATATGTGTATATAAGAGGTTATTGATAAACTTCTGAGGCAGAC
ATTTGTCTCGCTTTTTTTCATTTTTTGTGTTGTCTTATAAACTGACTGTTTTTCTTTGCTTGGA
TACTGTGATTCCAAAATAAATCTCATCCAAGCAAGTTAGAGTCCAGCCTAATCAAATGTCATA
ATTGTTGTACCTATTGAAAGTTTTTAAATAATAGATTTATTATGTAAATTATAGTATATGTAA
GTAGCTAATGAAGTAAAGATCATGAAGAAAGAAATTGATAGGTGTAAATGAGAGACCATGTAA
AATATGTAAATCTAGTACCTGAAATCCTTCAACAGATTTTATATAGCAACTGCTCTCTGC
AAGTAGTTAAACTAGAACTGGGCACATGGTAGAGGCTCACATGGGAGTTGTCCTCACCCCTG
TTAATCTCAAGAACTCTTATTTATAATAGGTTGCTTCTCTCTCAGAACTTTTATCTATTACT
TTTTTCTTCTTATGAGTATGTTTACTCTCAGAGTATCTATCTGATGTAGACAGTTGGTGATGC
TTCTGAGACTCAGAATGGTTTACTCTAACAAAACACTGTGCTGTCTATCCCTTGTAATTGCCT
ACTGTAATATGGATTTCACTTCTGAACAGTTTACAGCACAATATTTATTTTAAAGTGAATAAA
ATGTCCACAAGCAAAA

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FIGURE 94

MEEGGGGVRS LVPGGPVLLVLCGLLEASGGGRALPQLSDDIPFRVNWPGTEFSLPTTGVLYKE
DNYVIMTTAHKEKYKCILPLVTSGDEEEKDYKGPNPRELLEPLFKQSSCSYRIESYWTYEV
HGKHIRQYHEEKETGQKINIHEYLLGNMLAKNLLFEKEREAEKEKSNEIPTKNIEGQMTPEY
PVGMCNGTPCSLKQNRPRSSTVMYICHPEKHEILSVAEVTTCYEVVILTPLLCSHPKYRFR
ASPVNDIFCQSLPGSPFKPLTLRQLEQQEEILRVFPFRNKEGVGWWKYEFYCYGKHVHQYHEDK
DSGKTSVVVGTTWNQEEHIEWAKKNTARAYHLQDDGTQTVRMVSHFYNGNDICDITDKPRQVTV
KLKCKESDSPHAVTVYMLEPHSCQYILGVESPVICKILDTADENGLLSLPN

Important features of the protein:

Signal peptide:

amino acids 1-30

Glycosaminoglycan attachment site.

amino acids 28-32

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 337-341

N-myristoylation sites.

amino acids 6-12, 23-29, 29-35, 49-55, 141-147, 152-158, 192-198,
196-202

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 54-60

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FIGURE 95

TTCCGTTTCTGGGAGGAGTGAGGGGCAACGGGTCTGGAGAAAAAGGAAAAAGAAGGGCTCAGC
GCCTCCCCGCCGGGCGGTGGACAGAGGGGCACAGTTTCGGCAGGCGGGTGAGGTCTGCTGAGGG
CCCGCCGGAGATGTTTTTCCTTGTCGAGCACGGTGCAACCCCAGGTTACAGTTCCTCTGAGTCA
TCTCATCAATGCCTTCCATACACCAAAAAACACTTCTGTTTCTCTCAGTGGAGTGTCTAGTTTC
TCAAAACCAGCATCGAGATGTAGTTCTTGAGCATGAGGCTCCCAGCAGTGAGCCTTCACTTAA
CTTAAGGGACCTTGGATTATCTGAACTAAAAATTGGACAGATTGATCAGCTGGTAGAAAATCT
ACTTCCTGGATTTTGTAAAGGCAAAAACATTTCTTCCCATTGGCATAACATCCCATGTCTCTGC
ACAATCCTTCTTTGAAAATAAATATGGTAACTTAGATATATTTAGTACATTACGTTCTCTTG
CTTGTATCGACATCATTCAAGAGCTCTTCAAAGCATTTGTTTCAGATCTTCAGTACTGGCCAGT
TTTCATACAGTCTCGGGGTTTTTAAACCTTTGAAATCAAGGACACGACGTCTCCAGTCTACCTC
CGAGAGATTAGCTGAAACACAGAATATAGCGCCATCATTCTGTAAGGGGTTTTCTTTTGCGGGA
CAGAGGATCAGATGTTGAGAGTTTGGACAACTCATGAAAACCAAAAATATACCTGAAGCTCA
CCAAGATGCATTTAAACTGGTTTTGCGGAAGGTTTTCTGAAAGCTCAAGCACTCACACAAAA
AACCAATGATTCCCTAAGGCGAACCCGTCTGATTCTCTTCGTTCTGCTGCTATTTCGGCATTTA
TGGACTTCTAAAAAACCCATTTTTATCTGTCCGCTTCCGGACAACAACAGGGCTTGATTCTGC
AGTAGATCCTGTCCAGATGAAAAATGTCACCTTTGAACATGTTAAAGGGGTGGAGGAAGCTAA
ACAAGAATTACAGGAAGTTGTTGAATTCTTGAAAAATCCACAAAAATTTACTATTCTTGGAGG
TAAACTTCCAAAAGGAATTCTTTTAGTTGGACCCCCAGGGACTGGAAAGACACTTCTTGCCCCG
AGCTGTGGCGGGAGAAGCTGATGTTCTTTTTATTATGCTTCTGGATCCGAATTTGATGAGAT
GTTTGTGGGTGTGGGAGCCAGCCGTATCAGAAATCTTTTTAGGGAAGCAAAGGCGAATGCTCC
TTGTGTTATATTTATTGATGAATTAGATTCTGTTGGTGGGAAGAGAATTGAATCTCCAATGCA
TCCATATTCAAGGCAGACCATAAATCAACTTCTTGCTGAAATGGATGGTTTTAAACCCAATGA
AGGAGTTATCATAATAGGAGCCACAACTTCCCAGAGGCATTAGATAATGCCTTAATACGTCC
TGGTTCGTTTTGACATGCAAGTTACAGTTCAGGCCAGATGTAAAAGGTCGAACAGAAATTTT
GAAATGGTATCTCAATAAAATAAAGTTTGATCAATCCGTTGATCCAGAAATTATAGCTCGAGG
TACTGTTGGCTTTTTCCGGAGCAGAGTTGGAGAATCTTGTGAACCAGGCTGCATTTAAAGCAGC
TGTTGATGGAAAAGAAATGGTTACCATGAAGGAGCTGGAGTTTTCCAAAGACAAAATTCTAAT
GGGGCCTGAAAGAAGAAGTGTGGAAATTGATAACAAAAACAAAACCATCACAGCATATCATGA
ATCTGGTCATGCCATTATTGCATATTACACAAAAGATGCAATGCCTATCAACAAAGCTACAAT
CATGCCACGGGGGCCAACACTTGGACATGTGTCCCTGTTACCTGAGAATGACAGATGGAATGA
AACTAGAGCCCAGCTGCTTGCACAAATGGATGTTAGTATGGGAGGAAGAGTGGCAGAGGAGCT
TATATTTGGAACCGACCATATTACAACAGGTGCTTCCAGTGATTTTGATAATGCCACTAAAT
AGCAAAGCGGATGGTTACCAAATTTGGAATGAGTGAAAAGCTTGGAGTTATGACCTACAGTGA
TACAGGGAAACTAAGTCCAGAAACCCAATCTGCCATCGAACAAAGAAATAAGAATCCTTCTAAG
GGACTCATATGAACGAGCAAAACATATCTTGAAAACCTCATGCAAAGGAGCATAAGAATCTCGC
AGAAGCTTTATTGACCTATGAGACTTTGGATGCCAAAGAGATTCAAATTTGTTCTTGAGGGGAA
AAAGTTGGAAGTGAGATGATGATAACTCTCTTGATATGGATGCTTGCTGGTTTTATTGCAAGAATA
TAAGTAGCATTGCAGTAGTCTACTTTTACAACGCTTTCCCCTCATTCTTGATGTGGTGTAATT
GAAGGGTGTGAAATGCTTTGTCAATCATTTGTCACATTTATCCAGTTTGGGTTATTCTCATTA
TGACACCTATTGCAAATTAGCATCCCATGGCAAATATATTTTGAAAAATAAAGAAGTATCAG
GATTGAAAACAAAAA

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FIGURE 96

MFSLSSTVQPQVTVPLSHLINAFHTPKNTSVSLSGVSVSQNQHRDVVPEHEAPSSEPSLNLRD
LGLSELKIGQIDQLVENLLPGFCKGKNISSHWHTSHVSAQSFFENKYGNLDIFSTLRSSCLYR
HHSRALQSICSDLQYWPVFIQSRGFKTLKSRTRRLQSTSERLAETQNIAPSFVKGFLLRDRGS
DVESLDKLMKTKNIPEAHQDAFKTGFAEGFLKAQALTQKTNDSLRRLILFVLLLFGIYGLL
KNPFLSVRFRTTTGLDSAVDPVQMKNVTFEHVKGVEEAKQELQEVVEFLKNPQKFTILGGKLP
KGILLVGPPGTGKTLLARAVAGEADVPFYYASGSEFDEMFGVVGASRIRNLFREAKANAPCVI
FIDELDSVGGKRIESPMHPYSRQTINQLLAEMDGFKPNEGVIIIGATNFPEALDNALIRPGRF
DMQVTVPRPDVKGRTEILKWYLNKIKFDQSVDPEIIARGTVGFSGAELENLVNQAAKAAVDG
KEMVTMKELEFSKDKILMGPERRSVEIDNKNKTITAYHESGHAI IAYTKDAMPINKATIMPR
GPTLGHVSLLPENDRWNETRAQLLAQMDVSMGGRVAEELIFGTDHITGASSDFDNATKIAKR
MVTKFGMSEKLGVM TYSDTGKLSPETQSAIEQEIRILLRDSYERAKHILKTHAKEHKNLAEAL
LTYETLDAKEIQIVLEGKKLEVR

Important features of the protein:**Transmembrane domain:**

amino acids 238-259

N-glycosylation sites.amino acids 28-32, 90-94, 230-234, 278-282, 535-539, 584-588,
623-627**N-myristoylation sites.**

amino acids 35-41, 266-272, 286-292, 325-331, 357-363, 599-605

Amidation site.

amino acids 387-393, 709-713

ATP/GTP-binding site motif A (P-loop).

amino acids 322-330

AAA-protein family proteins

amino acids 315-336, 343-386, 405-451

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FIGURE 97

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAG**ATG**AAAGCCTCTAGT
CTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAG
GAGACAGAA**TAG**GAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGATTGTCTTTATGCATCCCC
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAAATATCTTTCTGCTATTGGATATATT
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTAT
ACAGTAAAAAAAACCTTGTAATTCTAGAAGAGTGGCTAGGGGGGTTATTCATTTGTAT
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC
TACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 98

MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSEIRGSVQAKDGNIDIR
ILRRTESLQDTKFPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSEFLTICKDLRLC
HAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE

Signal sequence:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 107-110, 140-143

N-myristoylation site.

amino acids 51-56

Interleukin 10:

amino acids 9-176

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FIGURE 99

[illegible]

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FIGURE 100

MRLLEWELLFLLFGPWLLRKAVSAQIPESGRPQYLGLRPAAAGAGAPGQQLPEPRSSDGLGVGR
AWSAWPTNHTGALARAGAAGALPAQRTKRKPSIKAARAKKIFGWGDFYFRVHTLKFSLLVTG
KIVDHVNGTFSVYFRHNSSSLGNLSVSIVPPSKRVEFGGVWLPGPVPHPLQSTLALLEGVLPGL
GPPLGMAAAAAGPGLGGSLGGALAGPLGGALGVPGAKESRAFNCHVEYEKTNRARKHREPLYD
PSQVCFTHTQSQAAWLCAKPFKVICIFVSFLSFDYKLVQKVC PDYNFQSEHPYFG

Important features of the protein:**Signal peptide:**

amino acids 1-22

Transmembrane domain:

amino acids 273-288

N-glycosylation sites.

amino acids 72-76, 133-137, 143-147, 149-153

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 93-97

N-myristoylation sites.amino acids 35-41, 58-64, 60-66, 81-87, 84-90, 184-190, 194-200,
203-209, 205-211, 206-212, 209-215, 217-223, 221-227, 224-230**Cytochrome b/b6 Qo site signature.**

amino acids 5-11

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FIGURE 101

AATGCCCC**ATG**CGCACCCACAGCTCGCGCTCCTGCAAGTGTTCTTTCTGGTGTTCCCCGATG
GCGTCCGGCCTCAGCCCTCTTCCTCCCCATCAGGGGCAGTGCCACGTCTTTGGAGCTGCAGC
GAGGGACGGATGGCGGAACCCCTCCAGTCCCCTTCAGAGGCGACTGCAACTCGCCCGGCCGTGC
CTGGACTCCCTACAGTGGTCCCTACTCTCGTGACTCCCTCGGCCCCCTGGGAATAGGACTGTGG
ACCTCTTCCCAGTCTTACCGATCTGTGTCTGTGACTTGACTCCTGGAGCCTGCGATATAAATT
GCTGCTGCGACAGGGACTGCTATCTTCTCCATCCGAGGACAGTTTTCTCCTTCTGCCTTCCAG
GCAGCGTAAGGTCTTCAAGCTGGGTTTGTGTAGACAACTCTGTTATCTTCAGGAGTAATCCC
CGTTTCCTTCAAGAGTTTTTCATGGATTCTAATGGAATCAGGCAGTTTTGTGTCCATGTGAACA
ACTCAAACCTAAACTATTTCCAGAAGCTTCAAAGGTCAATGCAACCAACTTCCAGGCCCTGG
CTGCAGAGTTTGGAGGCGAATCATTCACTTCAACATTCCAAACTCAATCACCACCATCTTTTT
ACAGGGCTGGGGACCCCATTTCTTACTTACTTCCCCAAGTGGTCTGTAATAAGCTTGCTGAGAC
AACCTGCAGGAGTTGGAGCTGGGGGACTCTGTGCTGAAAGCAATCCTGCAGGTTTCTAGAGA
GTAAAAGTACAACTTGCACTCGTTTTTTCAAGAACCTGGCTAGTAGCTGTACCTTGGATTGAG
CCCTCAATGCTGCCTCTTACTATAACTTCACAGTCTTAAAGGTTCCAAGAAGCATGACTGATC
CACAGAATATGGAGTTCCAGGTTCTGTAATACTTACCTCACAGGCTAATGCTCCTCTGTTGG
CTGGAAACACTTGTCAGAATGTAGTTTCTCAGGTCACCTATGAGATAGAGACCAATGGGACTT
TTGGAATCCAGAAAGTTTCTGTGAGTTTGGGACAAACCAACCTGACTGTTGAGCCAGGCGCTT
CCTTACAGCAACACTTCATCCTTCGCTTCAGGGCTTTTCAACAGAGCACAGCTGCTTCTCTCA
CCAGTCCTAGAAGTGGGAATCCTGGCTATATAGTTGGGAAGCCACTCTTGGCTCTGACTGATG
ATATAAGTTACTCAATGACCCTCTTACAGAGCCAGGGTAATGGAAGTTGCTCTGTAAAAGAC
ATGAAGTGCAGTTTGGAGTGAATGCAATATCTGGATGCAAGCTCAGGTTGAAGAAGGCAGACT
GCAGCCACTTGCAAGCAGGAGATTTATCAGACTCTTCATGGAAGGCCCAGACCAGAGTATGTTG
CCATCTTTGGTAATGCTGACCCAGCCCAGAAAGGAGGGTGGACCAGGATCCTCAACAGGCACT
GCAGCATTTCAGCTATAAACTGTACTTCCTGCTGTCTCATACCAGTTTCCCTGGAGATCCAGG
TATTGTGGGCATATGTAGGTCTCCTGTCCAACCCGCAAGCTCATGTATCAGGAGTTCGATTCC
TATACCAGTGCCAGTCTATACAGGATTCTCAGCAAGTTACAGAAGTATCTTTGACAACCTCTTG
TGAACCTTTGTGGACATTACCCAGAAGCCACAGCCTCCAAGGGGCCAACCCAAAATGGACTGGA
AATGGCCATTGCACTTCTTCCCTTCAAAGTGGCATTGAGCAGAGGAGTATTTCTCTCAAAAAT
GCTCAGTCTCTCCCATCCTTATCCTGTGCCTCTTACTACTTGGAGTTCTCAACCTAGAGACTA
TG**TGA**AGAAAAGAAAATAATCAGATTTTCAAGTTTTCCCTATGAGAACTCTGAGGCAGCCACTT
ATCTTGGCTAAATAGAACCTCACCTGCTCATGACCAGAGAGCATTTAGGATAATAGATGACCT
AACTGAAGGAATCCTTGTATATGAAAGGAGTTATTTTAGAAAAGCAATAAAAATATTTTATTC
ATCNTAAAAA

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FIGURE 102

M RTPQLALLQVFFLVFPDGVRPQPSSSPSGAVPTSLELQRGTDGGTLQSPSEATATRPVAVPGL
PTVVPTLVTPSAPGNRTVDLFFVLPICVCDLTPGACDINCCCDRDCYLLHPRTVFSFCLPGSV
RSSSWVCVDNSVIFRSNSPFPSRVFMDSNQIRQFCVHVNNNSNLNYFQKLQKVNATNFAQALAAE
FGGESFTSTFQTQSPPSFYRAGDPILTYFPKWSVISLLRQPAGVGAGGLCAESNPAGFLESKS
TTCTRFFKNLASSCTLDSALNAASYNFTVLKVPRSM TDFQNMEFQVFVILTSQANAPLLAGN
TCQNVVSQVTYIEIETNGTFGIQKVS VSLGQTNLTVEPGASLQQHFILRFRAFQQSTAASLTSP
RSGNPGYIVGKPELLALTDISYSMTLLQSQNGSCSVKRHEVQFGVNAISGCKLRLKKADCSH
LQQEIYQTLHGRPRPEYVAIFGNADPAQKGGWTRILNRHCSISAINCTSCCLIPVSLEIQVLW
AYVGLLSNPQAHVSGVRFLYQCQSIQDSQQVTEVSLTTLVNFVDITQKPQPPRGQPKMDWKWP
FDFPFKVAFSRGVFSQKCSVSPILILCLLLLGVLNLETM

Important features of the protein:**Signal peptide:**

amino acids 1-22

Transmembrane domains:

amino acids 484-505, 581-600

N-glycosylation sites.amino acids 78-82, 165-169, 179-185, 279-285, 331-337, 347-351,
410-414, 487-491**N-myristoylation sites.**

amino acids 30-36, 41-47, 124-130, 232-238, 236-242, 409-415

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 420-431

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FIGURE 103

CCTAATTCTCAAGGTGATGCTATTTAGGAAGTCATAACTCATGTGAGTGGAGCCATGTGGGAT
TAAGAAGTGATAGGAGAGCTTGCTGTCTGTCTCTGCTCTCCACTGTGTGAGGATACAACAGGA
AGACAGCCATCTGGTGAGGAAGAGAGGGCCCTCGCCAGATACCGGACCTGCTGACACCTTGAT
CTTGGACTIONCCCATCTTCCAGGAAGGCCTGACCTCAGTTGTTCCAGGGTAAAGAATTTGGGCA
GTGCCCACACCCACGCTGTTGGATAACATTTCTTCACCATAACCAGTGAGGGTGAATGTGTACA
CGCCCAGCTTCCTGCCTGTTACTCTCCACAGTATGCGAAGAATATCCCTGACTTCTAGCCCTG
TGCGCCTTCTTTTGTCTGCTGTTGCTACTAATAGCCTTGAGATCATGGTTGGTGGTCACT
CTCTTTGCTTCAACTTCACTATAAAATCATTTGTCCAGACCTGGACAGCCCTGGTGTGAAGCGC
AGGTCTTCTTGAATAAAAATCTTTTCCTTCAGTACAACAGTGACAACAACATGGTCAAACCTC
TGGGCCTCCTGGGGAAGAAGGTATATGCCACCAGCACTTGGGGAGAATTGACCCAAACGCTGG
GAGAAGTGGGGCGAGACCTCAGGATGCTCCTTTGTGACATCAAACCCAGATAAAGACCAGTG
ATCCTTCCACTCTGCAAGTCGAGATGTTTTGTCAACGTGAAGCAGAACGGTGCCTGGTGCAT
CCTGGCAGTTCGCCACCAATGGAGAGAAATCCCTCCTCTTTGACGCAATGAACATGACCTGGA
CAGTAATTAATCATGAAGCCAGTAAGATCAAGGAGACATGGAAGAAAGACAGAGGGCTGGAAA
AGTATTTTCAGGAAGCTCTCAAAGGGAGACTGCGATCACTGGCTCAGGGAATTCTTAGGGCACT
GGGAGGCAATGCCAGAACCGACAGGCAGAAGATCCACCTAGAGGTGATACCACGGCGGCGCAG
AGTTGTTACCTGTGGTCCTCGATCGCTGACAGCCTTGCTCCCCTGCTGTGTGTTCCCTGA
GTCAAGTGGAGGCGGAGCCTGCAATGAGCGGAGATCGCGCCTCTGCATTCCAGTCTTGGCAAC
AGAGCAAGACTCCGTCTCAAAAAAAAAAATTTTTTTTCAGTACATATTTTTTAAAGATAGG
GCTGGGCACAGCAGCTCACATCTATAATCCCAACACTTTGGGAGGCCTAGGCAGGAGGATCAC
TTGAGCCCAGGAATCTGAAGCTGCAGTGAGCCTTTGCTCGTGAGATTGTGGACCTATGATCCT
ACCACCAGCCCACCTGGTTCTAACACCCCCCTCCTCTATGTGTGAGAGGGAGAGAAGAAAAGTG
AGGGAGAAAAGAGAGATAAGCAAAGAACAGAGAGGAAAAATGGAAAATAAGAGGAAATTGGGG
GAATTAAACAGAGGGGAGGGCATGGATCCCCGGGAGTTAGAAGAGTAGCAGCTTGTGGATTAC
TACGCAGTGGAGGAAGAAGAGTTGTTGGAAATTATTTGAGAGGTAGTATAATCATTTGTGAGG
CAGTTTTCTGCATTACCATTTCTCACAGACTAAGTTACTCATAAGCAAACGTGCAATTCACA
TTACACTGAAATTCTTCCCTAATACATCATTTGCATTGGAATAAAGTACGGTTTTCAAACAAC
CTGATATAGCAGAACTGACTGTATAAATTATGTGAGCACAGTGCAAGTAATTCTTTGTTTGT
TGTTTTGTTTTTTTGGAGACAGAGTCTCACTCTATCTCCCAGGCTGGAGTGTAGTGGTGCATCC
CGGCTCACTGCAACCTCGATCTCCCAGGCTCAAGCGATTCCCCTGCCTCAGCCTCCTGAGTAG
CTGGGATTACAGGCATGAGCCACCACGCCCCGGCTAATTTTTGTATTTTTAGTAGAGACGGGGT
TTCACCCTGTTGGCCAGGCTGGTCTCGAACTACGGACCTCAGGTGATCTGCCCCCTCAGCCT
CTCAAAGTGCTGGGATTATAGCATGAGCCACTGAGCCCAGACACAAGTAGTTCTTTCTGATAA
ACACTTTAACTGAATGCA

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FIGURE 104

MRRISLTSSPVRLLLFLLLLLLIALEIMVGGHSLCFNFTIKSLSRPGQPWCEAQVFLNKNLFLQ
YNSDNNMVKPLGLLGKKVYATSTWGELTQTLGEVGRDLRMLLCDIKPQIKTSDPSTLQVEMFC
QREAERCTGASWQFATNGEKSLLFDAMNMTWTVINHEASKIKETWKKDRGLEKYFRKLSKGDC
DHWLREFLGHWEAMPEPTGRRST

Important features of the protein:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 11-30 (possible type II protein)

N-glycosylation site.

amino acids 36-39, 154-157

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 2-5, 182-185, 209-212

Casein kinase II phosphorylation site.

amino acids 86-89, 93-96, 142-145, 185-188

N-myristoylation site.

amino acids 46-51

Amidation site.

amino acids 77-80, 207-210

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FIGURE 105

TTTTCCGAGTGACCTTCTTGATGCTGGCTGTTTCTCTCACCGTTCCCCTGCTTGGAGCCATGA
TGCTGCTGGAATCTCCTATAGATCCACAGCCTCTCAGCTTCAAAGAACCCCCGCTCTTGCTTG
GTGTTCTGCATCCAAATACGAAGCTGCGACAGGCAGAAAGGCTGTTTGAAAATCAACTTGTTG
GACCGGAGTCCATAGCACATATTGGGGATGTGATGTTTACTGGGACAGCAGATGGCCGGGTGCG
TAAAACTTGAAAATGGTGAAATAGAGACCATTGCCCGGTTTGGTTTCGGGCCCTTGCAAACCC
GAGATGATGAGCCTGTGTGTGGGAGACCCCTGGGTATCCGTGCAGGGCCCAATGGGACTCTCT
TTGTGGCCGATGCATACAAGGGACTATTTGAAGTAAATCCCTGGAAACGTGAAGTGAACTGC
TGCTGTCCTCCGAGACACCCATTGAGGGGAAGAACATGTCCTTTGTGAATGATCTTACAGTCA
CTCAGGATGGGAGGAAGATTTATTTACCGATTCTAGCAGCAAATGGCAAAGACGAGACTACC
TGCTTCTGGTGATGGAGGGCACAGATGACGGGCGCCTGCTGGAGTATGATACTGTGACCAGGG
AAGTAAAAGTTTTATTGGACCAGCTGCGGTTCCCGAATGGAGTCCAGCTGTCTCCTGCAGAAG
ACTTTGTCCTGGTGGCAGAAACAACCATGGCCAGGATACGAAGAGTCTACGTTTCTGGCCTGA
TGAAGGGCGGGGCTGATCTGTTTGTGGAGAACATGCCTGGATTTCCAGACAACATCCGGCCCA
GCAGCTCTGGGGGGTACTGGGTGGGCATGTCGACCATCCGCCCTAACCCCTGGGTTTTCCATGC
TGGATTTCTTATCTGAGAGACCCCTGGATTAAAAGGATGATTTTTTAAGCTCTTTAGTCAAGAGA
CGGTGATGAAGTTTGTGCCGCGGTACAGCCTCGTCCTAGAACTCAGCGACAGCGGTGCCTTCC
GGAGAAGCCTGCATGATCCCGATGGGCTGGTGGCCACCTACATCAGCGAGGTGCACGAACACG
ATGGGCACCTGTACCTGGGCTCTTTCAGGTCCCCCTTCCTCTGCAGACTCAGCCTCCAGGCTG
TTTAGCCCTCCCAGATAGCTGCCCOCTGCCACGCAGGCCAGGAGTCTTCACACTCAGGCACCAG
GCCTGGTCCAGGAGGAGCTGTGGACACAGTTCGTGGTTCAAGTGTCCACATGCACCTGTTAGTC
CCTGAGAGGTGGTGGGAATGGCTGCTTCATTCCCTCGAGGATGCCCGGGCCCCACCTGGGCTTG
TCTTTCTGTTTAGAGGGGAAGTGTAACATATCTGCCATGAGGAACATAAATTCATGTAAAGCCA
TTTTCTCTTAAACAAAACAAAACCTTTCTAAGTACAATCATTCTCTAGGATTTGGGAAGCTCCT
TGCACTTGGAACAGGGCTCAGGTGGGTGGAGCAGTAAGGCACTACCCAGAGAGCTTGCTGCTG
CGGCCCTGTCCTGCGGCCTCAAAGTTCTTCTTTACTATATATAACGTGCGGTCATACCTTTCT
TCGTTGTGGTGGGGATGGAAGAGCAGAGGGAGCATGGCCCAGGGGTGTTGAGGCCAGCGGTGA
GAGCCGTGTTAGCCAAGACATGGAAGTGTGTTCTCAAGGGTTATGTGGGGCGTGGGCTCTCCA
TAGTGTGTATGAAAAGCTTGTTGACTCTAGCGGCTCAGAGAGGACTTTGCTGGGTTTCTTTCT
GTGAATATCTCCGTGCTGACCATGCTGGAATTGGATGATTCTGCAATTCGGGACCTACTGCAG
GGGTCCGTTTAGTAACGTCTTGTCTGTGATCTTTGTTCTTGACCTCTAGACCCCAAGATGTGA
ACAGTGCACGTGTTAATGTCATCTTTGCTCATGTGTTATAAGCCCCAAGTTGCTGTATATTTT
CACAAGTATGTCTACACACTGG

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FIGURE 106

MLAVSLTVPLLGA MMLLESPI DPQLSFKEPPLLLGVLHPNTKLRQAERLFENQLVGPESIAH
IGDVMFTGTADGRVVKLENGEIETIAREFGSGPCKTRDDEPVCGRPLGIRAGPNGTLFVADAYK
GLFEVNPWKREVKLLLSSETPIEGKNMSFVNDLTVTQDGRKIYFTDSSSKWQRRDYLLLVMEG
TDDGRLLEYDTVTREVKVLLDQLRFPNGVQLSPAEDFVLVAETTMARIRRVYVSGLMKGGADL
EVENMPGFPDNIRPSSSGGYWVGMSTIRPNPGFSMLDFLSERPWI KRMIFKLF SQETVMKFVP
RYSLVLELSDSGAFRRSLHDPDGLVATYISEVHEHDGHLYLG SFRSPFLCRLSLQAV

Important features of the protein:**Signal peptide:**

amino acids 1-13

Transmembrane domain:

amino acids 1-21 (possible type II)

N-glycosylation sites.

amino acids 116-119, 152-155

Casein kinase II phosphorylation sites.

amino acids 19-22, 27-30, 98-101, 146-149, 221-224, 286-289, 332-335

N-myristoylation sites.

amino acids 71-76, 92-97, 189-194, 244-249, 338-343

Amidation site.

amino acids 164-167

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FIGURE 107

AACGAAGCGTGCGCGCTTTGGTAACCGGCTAGAAATCCCGCACGCGCGCCTGCCTCCTCTCCC
CAGGCCTGAGCTGCCCCCTCCCACTGCCCTTTCCTTCTTCCCGCGAGTCAGAAGCTTCGCGAGGG
CCCAGAGAGGCGGTGGGGTGGGCGACCCCTACGCCAGCTCCGGGCGGGAGAAAGCCCACCCTCT
CCCGCGCCCCAGGAAACCGCCGGCGTTTCGGCGCTGCGCAGAGCC**ATG**GAAATTCCTCCTGGCTGG
AGACGCGCTGGGCGCGGCCCTTTTACCTGGCGTTCGTGTTCTGCCTGGCCCTGGGGCTGCTGC
AGGCCATTAAGCTGTACCTGCGGAGGCAGCGGCTGCTGCGGGACCTGCGCCCCCTTCCCAGCGC
CCCCACCCACTGGTTCCTTGGGCACCAGAAGTTTATTTCAGGATGATAACATGGAGAAGCTTG
AGGAAATTATTGAAAAATACCCCTCGTGCCCTTCCCTTCTGGATTGGGCCCTTTCAGGCATTTT
TCTGTATCTATGACCCAGACTATGCAAAGACACTTCTGAGCAGAACAGATCCCAAGTCCCAGT
ACCTGCAGAAATTCTCACCTCCACTTCTTGGAAAAGGACTAGCGGCTCTAGACGGACCCCAAGT
GGTTCAGCATCGTCGCCCTACTAACTCCTGGATTCCATTTTAACATCCTGAAAGCATACATTG
AGGTGATGGCTCATTCTGTGAAAATGATGCTGGATAAGTGGGAGAAGATTTGCAGCACTCAGG
ACACAAGCGTGGAGGTCTATGAGCACATCAACTCGATGTCTCTGGATATAATCATGAAATGCG
CTTTCAGCAAGGAGACCAACTGCCAGACAAACAGCACCCATGATCCTTATGCAAAAGCCATAT
TTGAACTCAGCAAAATCATATTTACCGCTTGTACAGTTTGTGTATCACAGTGACATAATTT
TCAAACCTCAGCCCTCAGGGCTACCGCTTCAGAAAGTTAAGCCGAGTGTTGAATCAGTACACAG
ATACAATAATCCAGGAAAGAAAGAAATCCCTCCAGGCTGGGGTAAAGCAGGATAACACTCCGA
AGAGGAAGTACCAGGATTTTCTGGATATTGTCTTTCTGCCAAGGATGAAAGTGGTAGCAGCT
TCTCAGATATTGATGTACACTCTGAAGTGAGCACATTCCTGTTGGCAGGACATGACACCTTGG
CAGCAAGCATCTCCTGGATCCTTTACTGCCTGGCTCTGAACCCTGAGCATCAAGAGAGATGCC
GGGAGGAGGTGAGGGGCATCCTGGGGGATGGGTCTTCTATCACTTGGGACCAGCTGGGTGAGA
TGTCGTACACCACAATGTGCATCAAGGAGACGTGCCGATTGATTCCCTGCAGTCCCGTCCATTT
CCAGAGATCTCAGCAAGCCACTTACCTTCCCAGATGGATGCACATTGCCTGCAGGGATCACCG
TGGTTCTTAGTATTTGGGGTCTTACCACAACCCTGCTGTCTGGAAAAACCCAAAGGTCTTTG
ACCCCTTGAGGTTCTCTCAGGAGAATTCTGATCAGAGACACCCCTATGCCTACTTACCATTCT
CAGCTGGATCAAGGAAGTGCATTGGGCAGGAGTTTGCCATGATTGAGTTAAAGGTAACCATTG
CCTTGATTCTGCTCCACTTCAGAGTGACTCCAGACCCACCAGGCCTCTTACTTTCCCCAACC
ATTTTATCCTCAAGCCCAAGAATGGGATGTATTTGCACCTGAAGAACTCTCTGAATGT**TAGA**
TCTCAGGGTACAATGATTAAACGTACTTTGTTTTTTCGAAGTTAAATTTACAGCTAATGATCCA
AGCAGATAGAAAGGGATCAATGTATGGTGGGAGGATTGGAGGTTGGTGGGATAGGGGTCTCTG
TGAAGAGATCCAAAATCATTCTAGGTACACAGTGTGTCAGCTAGATCTGTTTCTATATACT
TTGGGAGATTTTCAGATCTTTTCTGTTAAACTTTCACTACTATTAATGCTGTATACACCAATA
GACTTTCATATATTTTCTGTTGTTTTTAAATAGTTTTTCAGAATTATGCAAGTAATAAGTGCA
TGTATGCTCACTGTCAAAAATTCCCAACACTAGAAAATCATGTAGAATAAAAATTTTAAATCT
CACTTCACTTAGCCGACATTCCATGCCCTGACCAATCCTACTGCTTTTCTAAAAACAGAATA
ATTTGGTGTGCATTCTTTCAGACTTTTTCTTATACATTTTATATGTAGAAATGTAGCAATGTA
TTTGTATAGATGTGATCATTCCTATATTGTTATTGATTTTTTTCACCTAATAAAAATTCACCT
TATTCCTTAAAA

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FIGURE 108

MEFSWLETRWARPFYLAFFVFCALGLLQAIKLYLRRQRLLRDLRPFAPPTHWFLGHQKFIQD
DNMEKLEEIIEKYPRAPFFWIGPFQAFFCIYDPDYAKTLLSRTDPKSQYLQKFSPPLLKGKGLA
ALDGPKWFQHRRLTPEGFHFNILKAYIEVMAHSVMMMLDKWEKICSTQDTSVEVYEHINSMSL
DIIMKCAFSKETNCQTNSTHDPYAKAIFELSKII FHRLYSLLYHSDIIFKLSPQGYRFQKLSR
VLNQYTDITIIQERKKSLQAGVKQDNTPKRKYQDFLDIVLSAKDESGSSFSDIDVHSEVSTFLL
AGHDTLAASISWILYCLALNPEHQERCREEVRGILGDGSSITWDQLGEMSYTTMCIKETCRLI
PAVPSISRDL SKPLTFPDGCTLPAGITVVL SIWGLHHNPAVWKNPKVFDPLRFSQENS DQRHP
YAYLPFSAGSRNCIGQEFAMIELKVTIALILLHERVTPDPTRPLTFPNHFILKPKNGMYLHLK
KLSEC

Important features of the protein:**Signal peptide:**

amino acids 1-29

Transmembrane domains:

amino acids 310-330, 397-413, 459-473

N-glycosylation site.

amino acids 206-210

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 265-269, 504-520

N-myristoylation sites.

amino acids 25-31, 298-304, 353-359, 450-456, 456-462

Cytochrome P450 cysteine heme-iron ligand signature.

amino acids 447-457

Cytochrome P450 cysteine heme-iron ligand proteins.

amino acids 444-475

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FIGURE 109

GGCGTTCCGGGCCTCAACTTTGGCGTCGTGAGATTCTTGTGAGGCGTCTGCCTGGAAGCCGGC
AGCAATTTTGCTTCTTTAAAGAGAAAAAGAAGGCTAGGGACTCAGATTCCTGGATTCTGAGAT
CCAGACCAGCTCCTCCCAGACCTCTCCAGAAGAAGCCATGGGAACCCCTCGTATCCAGCATTT
GCTGATCCTCCTGGTCCTAGGAGCCTCCCTCCTGACCTCGGGCCTAGAGCTGTATTGTCAAAA
GGGTCTGTCCATGACTGTGGAAGCAGATCCAGCCAATATGTTTAACTGGACCACAGAGGAAGT
GGAGACTTGTGACAAAGGGGCACTTTGCCAGGAAACCATACTAATAATTAAAGCAGGGACTGA
GACAGCCATTTTGGCCACGAAGGGCTGCATCCCGGAAGGGGAGGAGGCCATAACAATTGTCCA
GCACTCTTCACCTCCCGGCCTGATCGTGACCTCCTACAGTAACTACTGTGAGGATTCCTTCTG
TAATGACAAAGACAGCCTGTCTCAGTTTTGGGAGTTCAGTGAGACCACAGCTTCCACTGTGTC
AACAACCCCTCCATTGTCCAACCTGTGTGGCTTTGGGGACCTGTTTCAGTGCTCCTTCTCTTCC
CTGTCCCAATGGTACAACCTCGATGCTATCAAGGAAAACCTTGAGATCACTGGAGGTGGCATTGA
GTCGTCTGTGGAGGTCAAAGGCTGTACAGCCATGATTGGCTGCAGGCTGATGTCTGGAATCTT
AGCAGTAGGACCCATGTTTGTGAGGGAAGCGTGCCACATCAGCTGCTCAACCTCGAAA
GACTGAAAATGGGGCCACCTGTCTTCCCATTCTCTGTTTGGGGGTTACAGCTACTGCTGCCATT
GCTGCTGCCATCATTATTCACCTTTTCCTAAGAGGCACTTCTGGGCCTGGGTCTGAGGACAT
CTTTTTTGA CTGGGAGCCTTCTTACTGTTGAGGTTCAACAAGCTGAGGAGTAGATGGGAATTT
GAGGGAGAATACAGAGATACTATGAACGTATTTGACATTTTAAATACAATTTCTGCTATAATT
TTTGTATGCAGTAGGCGTTACTAATAAACATTTCTGCTGTGA

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FIGURE 110

MGTPRIQHLLILLVLGASLLTSGLELYCQKGLSMTVEADPANMFNWTTEEVEETCDKGALCQET
ILLIKAGTETAILATKGCIP EGEEAITIVQHSSPPGLIVTSYSNYCEDSFNDKDSLSQFWEF
SETTASTVSTTLHCPTCVALGTCFSAPSLPCPNGTTRCYQGKLEITGGGIESSVEVKGCTAMI
GCRLMSGILAVGPMFVREACPHQLLTQPRKTENGATCLPIPVGWLQLLLPLLLPSFIHFS

Important features of the protein:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 184-201

N-glycosylation sites.

amino acids 45-49, 159-163

N-myristoylation sites.amino acids 31-37, 70-76, 99-105, 147-153, 160-166, 174-180,
175-181

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FIGURE 111

CGAGAAGAGGACAGAGGAGACTGAGCAAAGGGGGGTGGGCTCCAGGCGACCCCTAGCCCAATTCTGCCCTCCAT
 CCCAAGGGGCGAGAGAAATTGCTTTCTTTGCTGACTCCTACGAGGAAAAAAAAAAAAAAAAAAAAACCATTTTAA
 AGGGAAAGATAAACGGAGACGGAGGAAAGGTGGCAGCCAGATTACTTAGAGAGGCACAGAGGAGAGAGATCGGGG
 TGAGTCCGCCATGGGGACTCCCAGGGCCAGCACCCGCCGCTCCCCAGCTGCTGTTCTTAATTCTGCTGAGCTGT
 CCCTGGATCCAGGGTCTGCCCCCTGAAGGAGGAGGAGATATTGCCAGAGCCTGGAAGTGAGACCCCCACGGTGGCC
 TCTGAGGGCCCTGGCTGAAGTGTTCATGGGGCCCTGCTGAGGAGGGGGCCAGAGATGGGCTACCTGCCAGGATCT
 GATCCGGACCCACGCTAGCCACCCCTCCGGCCGGCCAGACTCTCGCAGTGGCCCTCCCTGCCACGGGCCACTGAG
 CCGGGACAGGGCCTCTGACAACAGCCGTCAACCCCTAACGGGGTCAAGGGGGCAGGCCCCACTGCCCCAGAACTG
 CTGACCCCGCCCCCAGGAACACAGCCCCACCCCAACCCAGCCCTGCCCTCCCCAGGGCCTCCCTTGGGCCTGAG
 GGAGGAGAGGAGAGACGACGACCAACCATCATCACCAAGACAACCTGTTACCCTACGGTGACCAAGCCAGCTTCTG
 TGTAATAACAACATCTCCGAGGGCGAAGGGTATGTGGAGTCTCCAGATCTGGGGAGCCCCGTCAGCCGCACCCCTG
 GGGCTCCTGGACTGCACTTACAGCATCCATGTCTACCCCTGGCTACGGCATTGAGATCCAGGTGCAGACGCTGAAC
 CTGTACAGGAAGAGGAGCTCCTGGTGTGGCTGGTGGGGGATCCCCAGGCCTGGCCCCCGACTCCTGGCCAAC
 TCATCCATGCTTGGAGAAGGACAAGTCCCTTCGGAGCCCAACCAACCGGCTGCTTCTGCACTTCCAGAGCCACGG
 GTCCCAAGGGGCGGTGGCTTCAGGATCCACTATCAGGCCTACCTCCTGAGCTGTGGCTTCCCTCCCGGCCGGCC
 CATGGGGACGTGAGTGTGACGGACCTGCACCCCTGGGGGCACTGCCACCTTTCAGTGTGATTCCGGGCTACCAGCTG
 CAGGGAGAGGAGACCCCTCATCTGCCTCAATGGCACCCGCCATCCTGGAACGGTGAAACCCCCAGCTGCATGGCA
 TCCTGTGGTGGCACCATCCACAATGCCACCCTGGGCCGCATCGTGTCCCCAGAGCCTGGGGGAGCCGTAGGGCCC
 AACCTCACCTGCCGTTGGGTCAATTGAAGCAGCTGAGGGGCGCCGGCTGCACCTGCACCTTGAAGGGTCTCGCTG
 GATGAGGACAATGACCGCTGATGGTGCCTCAGGGGGCAGCCCCCTATCCCCCGTGATCTATGATTGGGACATG
 GACGATGTCCCGAGCGGGGTCTCATCAGTGACGCCAGTCCCTCTACGTGGAGCTGCTGTGAGAGACACCTGCC
 AATCCCTGCTGTTAAGCCTTCGATTTGAAGCCTTTGAGGAGGATCGCTGCTTCGCCCTTCTCTGGCACATGGA
 AATGTCACTACCACGGACCCTGAGTATCGCCAGGGGCACTGGCAACCTTCTCGTGCCTCCAGGATATGCCCTG
 GAGCCCCCTGGCCCCCAATGCCATCGAATGTGTGGATCCACAGAACCCCACTGGAACGACACAGAGCCGGCC
 TGCAAAGCCATGTGTGGAGGGGAGCTGTCCGAACAGCTGGCGTGGTCTCTCTCCCGACTGGCCCCAGAGCTAT
 AGCCCCGGCCAAAGACTGCGTGTGGGGCGTGCACGTCCAGGAAGAGAAGCGCATCTTGCTCCAAGTTGAGATATTG
 AATGTGCGGGAAGGGGACATGCTGACGCTGTTCCAGCGGGACGGTCCCAGCGCCCGAGTCTTGGCCAGCTGCGG
 GGACCTCAGCCGCGCCGCGCCTTCTCTCCTCTGGGCCCGACCTCACACTGCAGTTTCAGGCACCGCCGGGCC
 CCAAATCCAGGCCTGGGCCAGGGCTTCGTATTGCACTTCAAAGAGGTCCCGAGGAACGACACGTGCCCCGAGCTG
 CCACCTCCGGAGTGGGGCTGGAGAACGGCATCCACGGGGACCTGATCCGGGGCAGGCTGCTCACCTACAGTGC
 GAGCCTGGCTACGAGCTGCTAGGCTCCGACATTCTCACTTGCCAGTGGGACCTGTCTTGGAGCGCCGCGCCGCC
 GCCTGCCAAAAGATCATGACTTGTGCTGACCCCTGGCGAGATTGCCAACGGGCACCGCACCGCCTCGGACGCCGGC
 TTCCCCGTTGGCTCCACGTCCAGTACCGCTGCCAGGGTACAGCCTCGAGGGGGCAGCCATGCTCACCTGC
 TACAGCCGGGACACAGGCACACCCAAGTGGAGCGATAGGGTCCCCAAATGCGCCTTGAAGTACGAGCCGTGCCCTG
 AACC CGGGGGTTCCCGAGAATGGCTACCAGACGCTGTACAAGCACCCTACCAGGCGGGCGAGTCTCTGCGCTTC
 TTCTGCTATGAGGGCTTTGAGCTTATCGGCGAGGTCACCATCACCTGTGTGCCCGGCCACCCCTCCAGTGGACC
 AGCCAGCCCCCACTCTGCAAAGTGACCCAGACACAGATCCATCACGGCAGCTGGAAGGGGGGAACCTGGCCCTG
 GCCATCCTGCTGCCCTTAGGCTTGGTCATTGTCTCGGCAGTGGCGTTTACATCTACTACACCAAGCTTCAGGGA
 AAGTCCCTTTTCGGCTTCTCGGGCTCCCACTCCTACAGCCCCATCACCGTGGAGTGGGACTTCAGCAACCCGCTG
 TATGAAGCTGGGGATACCGGGAGTATGAAGTTCCATCTGAACCCCAAGACTACAGCTGCAGGACCCAGGACGC
 CCCTCCCTCCTCATTCCGGGAGAGGGAAATACGGGACCCGGTCTCTGCCCTCCTGGCTGCCCTCCTCCCTGGCTG
 TGTAATAGTCTCCCTATCCACGAGGGGGCTTTGATGGCCCTGGAGATCCTACAGTAAATAAACAGCATCCTG
 CCGCCCAAAAA

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FIGURE 112

MGTPRAQHPPPPQQLFLILLSCPWIOGLPLKEEEILPEPGSETPTVASEALAEELLHGALLRRG
 PEMGYLPGSDPDPTLATPPAGQTLAVPSLPRATEPGTGPLTTAVTPNGVRGAGPTAPELLTTP
 PGTAPPPPPSPASPGPPLGPEGGEEETTTTIIITTTTIVTTTSPVLCNNNISEGEGYVESPD
 GSPVSRITLGLLDCTYSIHVYPGYGIEIQVQTLNLSQEEELLVLAGGGSFGLAPRLLANSSMLG
 EGQVLRSPNRLLLHFQSPRVPRGGGFRIHYQAYLLSCGFPPRPAHGDVSVTDLHPGGTATFH
 CDSGYQLQGEETLICLNTRPSWNGETPSCMASCGGTIHNATLGRIVSPEPGGAVGPNLTCRW
 VIEAAEGRRLHLHFERSLDEEDNDRLMVRSGGSPLSPVIYDSDMDDVPERGLISDAQSLYVEL
 LSETPANPLLLSLRFEAFEEEDRCFAPFLAHGNVTTTDPPEYRPGALATFSCLPGYALEPPGPN
 AIECVDPTEPHWNDTEPACKAMCGGELSEPAGVVLSPDWPPQSYSPGQDCVWGVHVQEEKRILL
 QVEILNVREGDMLTLFDGDGPSARVLAQLRGPQPRRRLSSGPDLTQFQAPPGPPNPGLGQG
 FVLHFKEVPRNDTCPELPPPEWGWRTASHGDLIRGTVLTYQCEPGYELLGSDILTCQWDLWS
 AAPPACQKIMTCADPGEIANGHRTASDAGFPVGSVQYRCLPGYSLEGAAMLTCSYRDTGTPK
 WSDRVPKCALKYEPCLNPGVPENGYQTLKYHHYQAGESLRFFCYEGFELIGEVTITCVPGHPS
 QWTSQPPCLKVTQTTDPSRQLEGGNLALAILLPLGLVIVLGSGVYIYYTKLQKSLFGFSGSH
 SYSPITVESDFSNPLYEAGDTREYEVSI

Important features of the protein:**Signal peptide:**

amino acids 1-27

Transmembrane domain:

amino acids 842-864

N-glycosylation sites.

amino acids 176-180, 222-226, 247-251, 332-336, 355-359, 373-377,
 473-477, 517-521, 641-645

Tyrosine kinase phosphorylation site.

amino acids 61-69

N-myristoylation sites.

amino acids 2-8, 84-90, 111-117, 114-120, 190-196, 198-204,
 235-241, 309-315, 333-339, 351-357, 472-478, 484-490, 528-534,
 626-632, 665-671, 775-781, 842-848

Amidation site.

amino acids 384-388

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23

CUB domain proteins profile.

amino acids 202-218, 376-392, 553-569

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FIGURE 113

GCCGCGGGCGGAGCTGCCTGCCGGTCCCGCGCCGCGCGTCCGCACTCCTCGGCCCTCGGGCGGGTUGATGGGACGG
 GGCGCCGCGGAGCAGGAGGGCGGCGCCCGTCCGGGGTGTCTCGGGCCGCGCGGGAGCCCACTGTGGGGCTCGGGCATG
 GCGGGCCGCGAGACCTGAGCTCTCCTCAGGGGAGCGGGGAGGCAGCTGCTGGCCGCGATGGGGACGGAGTGGGG
 CCGTCCGCGCCGCGCGGAGCCGTGAGCGCCGAGCCACCGCCGCGCTACCTCAGCCCTTCGCGAAGCGCCGGGCA
 GCTCGGGAACATGGCCCTGGAGCGGCTCTGCTCGGTCTCAAAGTGTTGTTAATAACAGTACTGGTAGTGGGAAGG
 GATTGCCGTGGGCCAAAAAACCAAGATGGACAAAATATTGGAATCAAGCATATTCTGCAACCCAGTGTGGCAT
 TTGGGTTCGAACCAGCAATGGAGGTCATTTTGTTCGCCAAATTATCCTGACTCATATCCACCAACAAGGAGTG
 TATCTACATTTTGGAGCTGCTCCACGTCAAAGAATAGAGTTGACCTTTGATGAACATTATTATATAGAACCATC
 ATTTGAGTGTGGGTTTGATCACTTGGGAAGTTCGAGATGGGCCATTGGGTTCTCTCCTCTTATAGATCGTTACTG
 TGGCGTGAAAAGCCCTCCATTAATTAGATCAACAGGGAGATTTCATGTGGATTAAAGTTTAGTTCTGATGAAGAGCT
 TGAAGGACTGGGATTTTCGAGCAAAATATTCAATTTATTCCAGATCCAGACTTTACTTACCTAGGAGGTATTTTAAA
 TCCCATTCCAGATTGTGAGTTCGAGCTCTCGGGAGCTGATGGAATAGTGGCTCTAGTCAGGTAGAACAAGAGGA
 GAAAACAAAACCAGGCCAAGCCGTTGATTGCATCTGGACCATTAAGCCACTCCAAAAGCTAAGATTTATTTGAG
 GTTCTTAGATTATCAAATGGAGCACTCAAATGAATGCAAGAGAACTTCGTTGCACTCTATGATGGAAGCAGTTC
 TATTGAAAACCTGAAGGCCAAGTTTTGCAGCACTGTGGCCAATGATGTAATGCTTAAACAGGAATTGGAGTGAT
 TCGAATGTGGGCAGATGAAGGTAGTCCGCTTAGCAGSTTTCGAATGCTCTTTACTTCCCTTTGTGGAGCCTCCCTG
 CACAAGCAGCACTTTCTTTTGGCATAGCAACATGTGCATCAATAATTCTTTAGTCTGTAATGGTGTCCAAAATTG
 TGCATACCCCTTGGGATGAAAATCATTGTAAAGAAAAGAAAAAGCAGGAGTATTTGAACAAATCACTAAGACTCA
 TGGAAACAATTATTGGCATTACTTCAGGGATTGTCTTGGTCTTCTCATTTATTTCTATTTTAGTACAAGTGAACA
 GCCTCGAAAAAAGGTATGGCTTGAACAAACCGCTTTTAATAAAAACCGGGTCCAAAGAAGTGTTTGATCCTCCTCA
 TTATGAAGTGTTTTCTACTAAGGGACAAAGAGATTTCTGCAGACCTGGCAGACTTGTGCGAAGAATTGGACAATA
 CCAGAAGATGGCGCGCTCCTCCACCGCCTCCCGCTGCATCCACGACCACCACTGTGGGTGCGAGGCCTCCAGCGT
 CAAACAAAGCAGGACCAACCTCAGTTCCATGGAACCTCCTTTCCGAAATGACTTTGCACAACCACAGCCAATGAA
 AACATTTAATAGCACCTTCAAGAAAAGTAGTTACACTTTCAAACAGGGACATGAGTGCCCTGAGCAGGCCCTGGA
 AGACCGAGTAATGGAGGAGATTCCCTGTGAAATTTATGTGAGGGGGCGAGAAGATTCTGCACAAGCATCCATATC
 CATTGACTTCTTAATCTTCTGCTAATGGTGTGTAATTCTTAGGGTGTGTACGTACGCAAGCTCCAGGGCACCAT
 ACTGTTTCCAGCAGCCAACCCCTTTCTCCCATCACAACACGAAAGACCTTGATTTACCGTTAACCTATTGTATGG
 TGATGTTTTTTATTTCTCTCAGGCAGTCTATATATGTTAAACCAATCAAGGAACCTTACTCTATTTCAGTGGAAACAAT
 AATCATCTCTATTGCTTGGTGTCAATTTATAGGAAGCACTGCCAGTTAAAGAGCATTAGAAGAGGTGGTTGGATGG
 AGCCAGGCTCAGGCTGCCTCTTCGTTTTAGCAACAAGAAGACTGCTCTTGACTGATAACAGCTCTGTCAATATTT
 TGATGCCACAATAAACTTGATTTTTTTTTTACATTCCTTTTATTTTTCCTTTCTCTAAATTTAATTTGTTTTATAA
 GCCTATCGTTTTTACCATTTTCATTTTCTTACATAAGTACAAGTGTTAATGTACCACATACTTCAGTATAGGCATT
 TGTTCTTGAGTGTGTCAAAATACAGCTAGTTACTGTGCCAATTAAGACCCAGTTGTATTTACCCATCTGTTTCT
 TCTTGGCTAATCTCTGTACTTCTGCCTTTTAATTACTGGGCCCTTATTCCTTATTTTCTGTGAGAAATAATAGAT
 GATATGATTTATTACCTTTCAATTATATTTTTCTCAGTTATACTAGAAAATTTCAATACTGGGATATATGTAC
 CATTGTCAGCTATGACTAAAAATTTGAAAAAGATAAAAAATTTCTAGCAAGCCTTTGAAGTTTACCAAGTATAGTC
 ACATTCAGTGACAGCCCATTCATTCCAGTAAAGAATCATTTTCACTTCTGGGAGAGGCCCTATAATTACATTTA
 TTTGCAATGTTTCTCTTCGCTAGATTGTTACATAGCTCCCATTTCTGTGGTTTTGCTTACAGCATATGGTAACCA
 AGGTTAGATGCCAGTTAAAAATTCCTTAGAAATTGGATGAGCCTTGAGATTGCTTCTTAACCTGGGACATGACATTT
 TTCTAGCTCTTATCAAGAATAACAACCTCCACTTTTTTTTAAACTGCACCTTTGACTTTTTTTATGGTATAAAAA
 CAATAATTTATAAACATAAAAGCTCATTGTGTTTTTTAGACTTTTGATATFATTTGATAGTGTACAACTTTATT
 AAATCAAGATGAAAGACCTACAGGACAGATTCCTTTCACTGTTTCATCAGTGGCTTTGTATGCAAATATGCTGT
 GTTGGACCTGGACGCTATAACTTATTGTAAAGACCTTGGAAATGTGGACATAAGCTCTTTCTTTCCCTTTTGTAC
 TGTATTTAGTTTTGTGATAAATTTTCACTGTGTGATATTTATGCTCTAAATCACTACACAAATCCCATATTTAAA
 TATACATTTGTACCTGAAAAAAA

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FIGURE 114

MALERLCSVLKVLLITVLVVEGIAVAQKTQDGQNIGIKHIPATQCGIWVRTSNGGHFASPNYP
DSYPPNKECIYILEAAPRQRIELTFDEHYIIEPSFECDHLEVRDGPFGFSPLIDRYCGVKS
PPLIRSTGRFMWIKFSSDEELEGLGFRAKYSFIPDPDFTYLGGILNPIPDQCQFELSGADGIVR
SSQVEQEEKTKPGQAVDCIWTIKATPKAKIYLRFLDYQMEHSNECKRNFVAVYDGSSSIENLK
AKFCSTVANDVMLKTGIGVIRMWADEGSRLSRFRMLFTSFVEPPCTSSTFFCHSNMCINNSLV
CNGVQNCAYPWDENHCKEKKKAGVFEQITKTHGTIIGITSGIVLVLLIISILVQVKQPRKKVM
ACKTAFNKTGFQEVFDPPHYELFSLRDKEISADLADLSEELDNYQKMRRSSTASRCIHDHHC
SQASSVKQSRTNLSSMELPFRNDFAQPQPMKTFNSTFKKSSYTFKQGHECPEQALEDRVMEEI
PCEIYVRGREDSAQASISIDF

Important features of the protein:**Signal peptide:**

amino acids 1-22

Transmembrane domain:

amino acids 348-369

N-glycosylation sites.

amino acids 311-315, 385-389, 453-457, 475-479

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 426-430, 479-483

N-myristoylation sites.amino acids 22-28, 32-38, 54-60, 186-192, 279-285, 318-324,
348-354, 352-358, 441-447

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FIGURE 115

GGTCTCTGTCCTTGGCTGTGGCTCCTGCGCTCTGGCTGAGCCATGTTCCCTTCTCCTCGCCCTC
CTCACTGAGCTTGGGAAGACTGCAAGCCCACGAAGGTTCTGAAGGAATATTTCTGCATGTCACA
GTTCCACGGAAGATTAAGTCAAATGACAGTGAAGTTTCAGAGAGGAAGATGATTTACATCATT
ACAATTGATGGACAACCTTACACTCTACATCTCGGAAAACAATCATTCTTACCCAGAACTTT
TTGGTTTATACATATAATGAACTGGATCTTTGCATTCTGTGTCTCCATATTTTATGATGCAT
TGCCATTACCAAGGATATGCTGCCGAATTTCCAAATTCATTTGTGACACTCAGTATATGTTCT
GGTCTCAGGGGATTTCTCCAGTTTGAAAATATCAGTTATGGAATTGAACCAGTAGAATCTTCA
GCAAGATTTGAGCATATAATTTATCAAATGAAAAATAATGATCCAAATGTATCCATTTTAGCA
GTAAATTACAGTCATATTTGGCAGAAAGACCAGCCCTACAAAGTTTCCTTTAAACTCACAGATA
AAAAATCTTTCAAAACTATTACCCCAATATCTGGAAATATACATTATAGTGGAAAAAGCTTTG
ATGTTTACCCAGTTCAAATTGACTGTTATACTGTCTTCCTTGGAATTGTGGTCAAATGAAAAC
CAGATTTCCACCAGTGGGGATGCTGATGATATATTACAAAGATTTTTTGGCATGGAAACGGGAC
TATCTCATCCTACGGCCCCATGACATAGCATACTTACTTGTTTACAGGAAACATCCTAAATAT
GTGGGAGCAACATTTCTGGCACCGTATGCAATAAAAGCTATGATGCAGGTATTGCTATGTAT
CCAGATGCAATAGGTTTGGAGGGATTTTCGGTTATTATAGCTCAACTGCTTGGCCTTAATGTA
GGATTAACATATGATGACATCACTCAGTGTCTGTCTGAGAGCTACATGCATCATGAATCAT
GAAGCAGTGAGTGCCAGTGGTAGAAAGATTTTAGCAACTGCAGCATGCACGACTATAGATAT
TTTGTTCCAAATTTGAGACTAAATGCCCTCAGAAGCTTTCAAATTTGCAACCATTACATCAA
AATCAACCAGTGTGTGGTAATGGGATTTTGGAAATCCAATGAAGAATGTGACTGTGGTAATAAA
AATGAATGTCAATTTAAGAAGTGCTGTGATTATAACACATGTAAACTGAAGGGCTCAGTAAAA
TGTGGTTCTGGACCATGTTGTACATCAAAGTGTGAGTTGTCAATAGCAGGCACTCCATGTAGA
AAGAGTATTGATCCAGAGTGTGATTTTACAGAGTACTGCAATGGAACCTCTAGTAATTGTGTT
CCTGACACTTATGCACTGAATGGCCGTTTGTGCAAGTTGGGAACTGCCTATTGCTATAACGGA
CAATGTCAAACACTGATAACCACTGTGCCAAGATATTTGGAAAAGGTGCTCAAGGTGCTCCA
TTTGCCTGTTTTAAAGAAGTTAATTCTCTGCATGAAAGATCTGAAAACCTGTGGTTTTAAAAAT
TCACAACCATTACCTTGTGAACGGAAGGATGTTCTCTGTGGAAAATTAGCTTGTGTTAGCCA
CATAAAAATGCTAATAAAAAGTGACGCTCAATCTACAGTTTATTCATATATTCAAGACCATGTA
TGTGTATCTATAGCCACTGGTTCCCTCCATGAGATCAGATGGAACAGACAATGCCTATGTGGCT
GATGGCACCATGTGTGGTCCAGAAATGTACTGTGTAAATAAAAACCTGCAGAAAAGTTCATTTA
ATGGGATATAACTGTAATGCCACCACAAAATGCAAAGGGAAAGGGATATGTAATAATTTTGGT
AATTGTCAATGCTTCCCTGGACATAGACCTCCAGATTGTAAATTCAGTTTGGTTCCCCAGGG
GGTAGTATTGATGATGGAAATTTTCAGAAATCTGGTGACTTTTATACTGAAAAGGCTACAAT
ACACACTGGAACAACCTGGTTTATTCTGAGTTTCTGCATTTTCTGCCGTTTTTCATAGTTTTC
ACCACTGTGATCTTTAAAAGAAATGAAATAAGTAAATCATGTAACAGAGAGAATGCAGAGTAT
AATCGTAATTCATCCGTTGTATCAGAAAGCGATGACGTGGGACATTAATATTGCACAGAACTT
CCATAGCAAATAACCTAAAGGAACGAATGTGCTTTATTTATAACCTTACGTTATCCCCAATGC
ATTGTAAATGTCAAACCTTTGGAAAATAAAGCCTGCGTGCCCTCCC

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FIGURE 116

MFLLLALLTELGRLQAHEGSEGI FLHVTVPRKIKSNDSEVSEKMIYIITIDGQPYTLHLGKQ
SFLPQNFLVYTYNETGSLHSVSPYFMMHCHYQGYAAEFPNSEFVTLCSGLRGFLQFENISYG
IEPVESARFEHIIYQMKNNDPNVSI LAVNYSHIWQKDQPYKVPLNSQIKNLSKLLPQYLEIY
IIVEKALMFTQFKLTVILSSLELWSNENQISTSGDADDILQREFLAWKRDYLILRPHDIAYLLV
YRKHPKYVGATFPGTVCNKS YDAGIAMYPDAIGLEGFSVIIAQLLGLNVGLTYDDITQCFCLR
ATCIMNHEAVSASGRKIFSNCSMHDYRYFVSKFETKCLQKLSNLQPLHQNPVCGNGILESNE
ECDCGNKNECQFKKCCDYNTCKLKGSVKCGSGPCCTSKCELSIAGTPCRKSIDPECDFTEYCN
GTSSNCVPDITYALNGRLCKLGTAYCYNGQCQTTDNQCAKIFGKGAQGAPFACFKEVNSLHERS
ENCGFKNSQPLPCERKDVLCGKLACVQPHKNANKSDAQSTVYSYIQDHVCVSIATGSSMRSDG
TDNAYVADGTMCGPEMYCVNKTCKRVHLMGYNCNATTKCKGKGICNNFGNCQCFPGHRPPDCK
FQFGSPGGSIDDGNFQKSGDFYTEKGYNTHWNNWFILSFCIFLPFFIVFTTVIFKRNEISKSC
NRENAEYNRNSSSVVSESDDVGH

Important features of the protein:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 665-684

N-glycosylation sites.amino acids 36-39, 76-79, 122-125, 149-152, 156-159, 177-180,
270-273, 335-338, 441-444, 537-540, 587-590, 601-604, 703-706**Casein kinase II phosphorylation sites.**amino acids 74-77, 208-211, 221-224, 304-307, 337-340, 346-349,
376-380, 415-418, 499-502, 639-642, 708-711**Tyrosine kinase phosphorylation site.**

amino acids 243-249

N-myristoylation sites.amino acids 53-58, 79-84, 266-271, 298-303, 372-377, 403-408,
408-413, 442-447, 462-467, 469-474, 488-493, 567-572, 610-615,
616-621, 634-639**Amidation site.**

amino acids 328-331

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FIGURE 117

CCCACGCGTCCGCGGACGCGTGGGGCTCAGTGGGCGTCGCGCGAAGGCTAAGGGAGTGTGGCG
GGCGGCTCCGGGAGCCAAC**ATG**CCTCGGTATGCGCAGCTGGTCATGGGCCCCGCGGGCAGCGG
GAAGAGCACCTACTGTGCCACCATGGTCCAGCACTGTGAAGCCCTCAACCGGTCTGTCCAAGT
TGTAACCTGGATCCAGCAGCAGAACACTTCAACTACTCCGFGATGGCTGACATCCGGGAAGT
GATCGAGGTGGATGATGTAATGGAGGATGATTCTCTGCGATTCCGGTCCCAACGGAGGATTGGT
ATTTTG CATGGAGTACTTTGCCAATAATTTTGACTGGCTGGAGAACTGTCTTGGCCATGTAGA
GGACGACTATATCCTTTTTGATTGTCCAGGTCAGATTGAGTTGTACACTCACCTGCCTGTGAT
GAAACATCTGGTCCAGCAGCTCGAGCAGTGGGAGTTCCGAGTCTGTGGAGTTTTTCTTGTTGA
TTCTCAGTTCATGGTGGAGTCATTCAAGTTTATTTCTGGCATCTTGGCAGCCCTGAGTGCCAT
GATCTCTCTAGAAATTCGCAAGTCAACATCATGACAAAATGGATCTGCTGAGTAAAAAGC
AAAAAAGGAAATTGAGAAATTTTGTAGATCCAGACATGTATTCTTTATTAGAAGATTCTACAAG
TGACTTAAGAAGCAAAAATTCAAGAACTGACTAAAGCTATATGTGGACTGATTGATGACTA
CAGCATGGTTCGATTTTTACCTTACGATCAGTCAGATGAAGAAAGCATGAACATTGTATTGCA
GCATATTGATTTTGCCATTCAATATGGAGAAGACCTAGAATTTAAAGAACCBAAGGAACGTGA
AGATGAGTCTTCCTCTATGTTTGACGAATATTTTCAAGAATGCCAGGATGAAT**TGA**AGAGTTTA
CTAAAAGTAACCATCTAAAGAGCTTGTGGCCAAACCAGCAGAACATTCTTCTCTTCAAAGGAT
GCAATAGTAGAAAGCTACTTATTTTAATGAAAAAAGTAAACTTCGTTCTTTATCAGCCTCA
TGCCTGAATCAAATTTTTAATTATCTGAAACTGCTGCTGTTTAAAGTGGAATCTTTTAGTAT
TATAACAGCATCACTTTAGATTTTGTAAGTCAAAATTGAAATGAATGCACATAGATTTATATA
TAAATTAGCACCTGAGCTAAGGTTAAGGCCGGTCTAAACTTATTTTCACTTTTTGTATTATTT
TTGAGATGCAGGAATTACTGTAAACAAAATATGTATGTCCGAAGGGAAAAAGCTGCAAGGATAT
ATATAAGACCACTGCTTATCTGTATCTTCCCATTTTCCTATATTGAAAATGTATATTATTTAT
ATAACTTAAAAAGTAAAAATAACTATGTTTTGAGAT

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FIGURE 118

MPRYAQLVMGPAGSGKSTYCATMVQHCEALNRSVQVVNLDPAAEHFNYSVMADIRELIEVDDV
MEDDSLRFPGPNGGLVFCMEYFANNFDWLENCGLGHVEDDYILFDCPGQIELYTHLPVMKHLVQQ
LEQWEFRVCGVFLVDSQFMVESFKFISGILAALSAMISLEIPQVNIMTKMDLLSKKAKKEIEK
FLDPDMYSLLEDSTSDLRSKKFKKLTKAICGLIDDYSMVRELPYDQSDEESMNIVLQHIDFAI
QYGEDLEFKEPKEREDESSMFDEYFQECQDE

Important features of the protein:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 151-170

N-glycosylation sites.

amino acids 31-35, 47-51

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 212-216

Tyrosine kinase phosphorylation site.

amino acids 189-197

N-myristoylation sites.

amino acids 13-19, 76-82, 154-160

ATP/GTP-binding site motif A (P-loop).

amino acids 10-18

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FIGURE 119

GGGCGCTGGGAGACACCGGACGCCCCGCTCGGCTGCGCTGCGGCTCAGGCCCCCGCTCGGGCCC
GACCCGCTCGGTACCGCCGGCTCGGGCGCGCACCTGCCGGCTGCGGCCCCAGGGCCATGCGG
AGGCCACGAGGAGGCCGGCGGCCACGCGCATCCCGTAGCCAGGTGGCCCAGGTCTGCACCG
CGGCGGCCTCGGCGCC**ATG**GAGCCCCCGTATTGCTGACGGCGCACTACGATGAGTTCCAAGA
GGTCAAGTACGTGAGCCGCTGCGGCGCGGGGGGCGCGCGGGGGCTCCCTGCCCCGGGCTT
CCCGTTGGGCGCTGCGCGCAGCGTCACCGGGGCCCGGTCCGGGCTGCCGCGCTGGAACCGGCG
CGAGGTGTGCTGCTGTCGGGGCTGGTGTTCGCCGCCGGCCTCTGCGCCATTCTGGCGGCTAT
GCTGGCCCTCAAGTACCTGGGCCCGGTGCGGGCCGGCGGGCGGCGCTGTCCCGAGGGCTGCCC
TGAGCGCAAGGCCCTTCGCGCGCGCCGCTCGCTTCCTGGCCGCCAACCTGGACGCCAGCATCGA
CCCATGCCAGGACTTCTACTCGTTGCGCTGCGGCGGTTGGCTGCGGCGCCACGCCATCCCCGA
CGACAAGCTCACCTATGGCACCATCGCGGCCATCGGCGAGCAAAACGAGGAGCGCCTACGGCG
CCTGCTGGCGCGGGCCCCGGGGTGGGCCTGGCGGCGCGGCCAGCGCAAGGTGCGCGCCTTCTT
CCGCTCGTGCTCGACATGCGCGAGATCGAGCGACTGGGCCCCGCGACCCATGCTAGAGGTCAT
CGAGGACTGCGGGGGCTGGGACCTGGGCGGCGCGGAGGAGCGTCCGGGGGTGCGGCGCGGATG
GGACCTCAACCGGCTGCTGTACAAGGCGCAGGGCGTGTACAGCGCCGCCGCGCTCTTCTCGCT
CACGGTCAGCCTGGACGACAGGAACCTTCGCGCTACGTTCATCCGCATTGACCAGGATGGGCT
CACCTGCCAGAGAGGACCCTGTACCTCGCTCAGGATGAGGACAGTGAGAAGATCCTGGCAGC
ATACAGGGTGTTTCATGGAGCGAGTGCTCAGCCTCCTGGGTGCAGACGCTGTGGAACAGAAGGC
CCAAGAGATCCTGCAAGTGGAGCAGCAGCTGGCCAACATCACTGTGTGAGAGTATGACGACCT
ACGGCGAGATGTCAGCTCCATGTACAACAAGGTGACGCTGGGGCAGCTGCAGAAGATCACCCC
CCACTTGCGGTGGAAGTGGCTGCTAGACCAGATCTTCCAGGAGGACTTCTCAGAGGAAGAGGA
GGTGGTGCTGCTGGCGACAGACTACATGCAGCAGGTGTGCGAGCTCATCCGCTCCACACCCCA
CCGGGTCTGCACAACTACCTGGTGTGGCGCGTGGTGGTGGTCTGAGTGAACACCTGTCCCC
GCCATTCCGTGAGGCACTGCACGAGCTGGCACAGGAGATGGAGGGCAGCGACAAGCCACAGGA
GCTGGCCCCGGGTCTGCTTGGGCCAGGCCAATCGCCACTTTGGCATGGCGCTTGGCGCCCTCTT
TGTACATGAGCACTTCTCAGCCGCCAGCAAAGCCAAGGTGCAGCAGCTAGTGGAAGACATCAA
GTACATCCTGGGCCAGCGCCTGGAGGAGCTGGACTGGATGGACGCCGAGACCAGGGCTGCTGC
TCGGGCCAAGCTCCAGTACATGATGGTGATGGTGGCTACCCGGACTTCTGCTGAAACCCGA
TGCTGTGGACAAGGAGTATGAGTTTGGAGGTCCATGAGAAGACCTACTTCAAGAACATCTTGAA
CAGCATCCCCCTCAGCATCCAGCTCTCAGTTAAGAAGATTCCGGCAGGAGGTGGACAAGTCCAC
GTGGCTGCTCCCCCACAGGCGCTCAATGCCTACTATCTACCCAACAAGAACCAGATGGTGTT
CCCCGCGGGCATCCTGCAGCCACCCCTGTACGACCCTGACTTCCACAGTCTCTCAACTACGG
GGGCATCGGCACCATCATTTGGACATGAGCTGACCCACGGCTACGACGACTGGGGGGGGCCAGTA
TGACCGCTCAGGGAACCTGCTGCACTGGTGGACGGAGGCCTCCTACAGCCGCTTCTGCGGAA
GGCTGAGTGCATCGTCCGTCTCTATGACAACTTCACTGTCTACAACCAGCGGGTGAACGGGAA
ACACACGCTTGGGGAGAACATCGCAGATATGGGCGTCTCAAGCTGGCCTACCACGCCCTATCA
GAAGTGGGTGCGGGAGCACGGCCCAGAGCACCCACTTCCCCGGCTCAAGTACACACATGACCA
GCTCTTCTTCATTGCCTTTGCCCAGAACTGGTGCATCAAGCGGCGGTGCGAGTCCATCTACCT
GCAGGTGCTGACTGACAAGCATGCCCTGAGCACTACAGGGTGTGGGCGAGTGTGTCCCAGTT
TGAGGAGTTTGGCCGGGCTTCCACTGTCCCAAGGACTCACCCATGAACCTGCCCACAAGTG
TTCCGTGTGG**TG**AGCCTGGCTGCCCCGCTGCACGCCCCCACTGCCCCCGCACGAATCACCTCC
TGCTGGCTACCGGGGGCAGGCATGCACCCGGTGCCAGCCCCGCTCTGGGCACCACTGCCTTCC
AGCCCCCTCAGGACCCGGTCCCCCTGCTGCCCTCACTTCAGGAGGGGGCTGGAGCAGGGTGA
GGCTGGACTTTGGGGGGCTGTGAGGGAAATATACTGGGGTCCCCAGATTCTGCTCTAAGGGGG
CCAGACCCCTCTGCCAGGCTGGATTGTACGGGGCCCCACCTTCGCTGTGTTCTTGCTGCAAAGTC
TGGTCAATAAATCACTGCACTGTTAAAAA

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FIGURE 120

MEPPYSLTAHYDEFQEVKYVSRGAGGARGASLPPGFPLGAARSVTGARSGLPRWNRREVCLL
 SGLVFAAGLCAILAAMLALKYLGPVAAGGGACPEGCPEKAFARAARFLAANLDASIDPCQDF
 YSFACGGWLRRAIPDDKLTGTIAAIGEQNEERLRRLRLARPGGGPGGAAQRKVRAFFRSCLD
 MREIERLGFRPMLLEVIEDCGGWDLGGAEEERPGVAARWDLNRLLYKAQGVYSAAALFSLTVSLD
 DRNSSRYVIRIDQDGLTLPERTLYLAQDEDESEKILAAAYRVFMERVLSLLGADAVEQKAQEILQ
 VEQQLANITVSEYDDLRRDVSSMYNKVTLGQLQKITPHLRWKWLLDQIFQEDFSEEEVVLLA
 TDYMQQVSQILIRSTPHRVLHNYLVWRVVVVLSEHLSPPFREALHELAQEMEGSDKPELARVC
 LGQANRHFGMALGALFVHEHFSAAASKAKVQQLVEDIKYILGQRLEELDWMDAETRAAARAKLQ
 YMMVMVGYPDFLLKPDADVKEYEFEVHEKTYFKNILNSIPFSIQLSVKKIRQEVDKSTWLLPP
 QALNAYYLPNKNQMVFPAFILQPTLYDPDFPQSLNYGGIGTIIGHELTHGYDDWGGQYDRSGN
 LLHWWTEASYSRFLRKAECIVRLYDNFTVYNQRVNGKHTLGENIADMGVKLKAYHAYQKWVRE
 HGPEHPLRLKYTHDQLFFIAFAQNWCIKRRSQSIYLOVLTDKHAPEHYRVLGVSVSQFEEFGR
 AFHCPKDSMPNPAHKCSVW

Important features of the protein:**Transmembrane domain:**

amino acids 64-88

N-glycosylation sites.

amino acids 255-259, 322-326, 656-660

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 722-726

N-myristoylation site.amino acids 24-30, 26-32, 27-33, 40-46, 47-53, 65-71, 148-154,
169-175, 170-176, 237-243, 450-456, 604-610, 607-613**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 85-96

Prenyl group binding site.

amino acids 772-777

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 609-619

Neutral zinc metallopeptidases, zinc-binding region proteins.

amino acids 609-619

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FIGURE 121

CGGACTGCCCCGACCGCGCGATGGAGTCGACCGGCAGCGTCGGGGAGGCCCCGGGCGGACCCC
GGGTGCTGGTGGTGGGCGGCGGCATCGCGGGGCTGGGCGCGGCGCAGAGGCTCTGCGGCCACT
CCGCCTTCCCGCACCTGCGGGTCCTGGAGGCCACGGCCCCGCGCCGGGGGCGCATCCGCTCGG
AGCGCTGCTTCGGTGGCGTGGTGGAGGTGGGCGCGCACTGGATCCATGGGCCCTCCCGGGGTA
ACCCCGTCTTCCAGCTGGCTGCTGAGTACGGGCTGCTGGGGGAGAAGGAGCTGTCCAGGAGA
ACCAGCTGGTGGAGACCGGGGGTCACGTGGGCCTGCCCTCCGTGAGCTACGCCAGCTCCGGGG
CCAGCGTGAGCCTCCAGCTGGTGGCGGAGATGGCGACTCTGTTCTACGGCCTGATAGACCAGA
CCCGGGAGTTCCTGCACGCTGCAGAGACCCCGGTGCCAGCGTCGGGGAGTACCTCAAGAAGG
AGATTGGCCAGCACGTGGCCGGCTGGACAGAGGATGAGGAGACCAGGAAGCTGAAGCTGGCCG
TCCTGAACCTCTTCAACCTGGAATGCTGTGTGAGCGGCACCCACAGCATGGACCTGGTGG
CCCTGGCACCCCTTTGGGGAGTATACCGTGCTGCCGGGGCTGGACTGCACCTTTTCTAAGGGCT
ATCAAGGACTCACAACTGCATGATGGCCGCCCTGCCGGAGGACACTGTAGTTTTTGAGAAGC
CTGTGAAGACCATCCACTGGAACGGGTCCTTCCAGGAGGCAGCCTTTCCCGGGGAGACCTTTC
CAGTGTCGGTAGAGTGTGAGGATGGAGACCGGTTCCTGGCGCACCATGTCATCGTCACCGTGC
CCTTAGGTTTTCTTAGGGAACATTTGGACACCTTCTTTGACCCTCCCCTGCCGGCTGAGAAGG
CAGAAGCAATCAGGAAGATAGGCTTTGGGACCAACAACAAAATCTTCCTGGAGTTTGAGGAGC
CCTTCTGGGAGCCAGACTGCCAGCTGATCCAGCTGGTGTGGGAGGACACGTGCCCCCTGGAGG
ATGCTGCCCCCTGAGCTACAGGACGCCTGGTTCGGGAAGCTCATTGGCTTTGTGGTCCTGCCTG
CCTTTGCGTCTGTCCACGTTCTCTGTGGGTTCATTGCCGGA CTTGAGTCTGAGTTCATGGAGA
CTCTGTCCGATGAAGAAGTACTTCTGTGTCTCACCCAAGTGCTCCGGAGAGTGACAGGAAACC
CACGGCTCCCCGCGCCCAAGAGCGTCCTGCGGTCTCGCTGGCACAGCGCCCCGTACACTAGGG
GGTCCTACAGCTACGTGGCCGTGGGCAGTACTGGGGGCGACCTGGACCTGCTGGCTCAGCCCC
TCCCTGCAGACGGCGCCGGCGCCCAGCTCCAGATCCTGTTTGCGGGGGAAGCCACACATCGCA
CGTTTTACTCCACGACGCACGGGGCTCTGCTGTGCGGATGGAGGGAGGCCGACCGCCTCCTCA
GTCTGTGGGCCCCGAGGTGCAGCAGCCCAGGCCGAGGCTCTAGCTGGGCCCAGCCTACTCTG
TTCCACCCGTGTGCGGGGTAGGCTGGGACCGTCATTTCTTCTGACAGATTTAGTCTGGCTTG
AAATTTGGGGATGTTAATGAGGGTCCTCTGGTTTTTGGTAACCAGGGCCACCTTCTCAGTTCT
TGTGTCTGTTATTGGAGTCTGGCCAGGGTTGACTTGAGCTGAGACACCAGATGCTCACGGAGA
TGCTGGACACATAAAGCAAGTTACAGCCACAAAAAAAAAAAAA

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FIGURE 122

MESTGSGVEAPGGPRVLVVGGGIAGLGAAQRLCGHSAFPHLRVLEATARAGGRIRSERCFGGV
VEVGAHWIHGPSRGNPVFQLAAEYGLLGEKELSQENQLVETGGHVGLPSVSYASSGASVSLQL
VAEMATLFYGLIDQTREFLHAAETPVPSVGEYLLKKEIGQHVAGWTEDEETRKLKLAVLNSFFN
LECCVSGTHSMDLVALAPFGEYTVLPGLDCTFSKGYQGLTNCMMAALPEDTVVFEKPKVTIHW
NGSFQEAAPFGETFPVSVECEDGDRFPAHHVIVTVPLGFLREHLDTFDPPLPAEKAEAIRKI
GFGTNNKIFLEFEEPPWEPCQLIQLVWEDTSPLEDAAPELQDAWFRKLIGFVVLPAFASVHV
LCGFIAGLESEFMETLSDEEVLLCLTQVLRRTGNPRLPAPKSVLRSRWHSAPYTRGSYSYVA
VGSTGGDLDLAQLPADGAGAQLQILFAGEATHRTFYSTTHGALLSGWREADRLLSLWAPQV
QQPRPRL

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 364-385

N-glycosylation site.

amino acids 253-257

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 408-412

N-myristoylation sites.amino acids 20-26, 21-27, 25-31, 105-111, 119-125, 164-170,
216-222, 227-233, 443-449, 484-490**Aminooxidase Flavin containing amine oxidase:**

amino acids 23-497

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FIGURE 123

CGGACGCGTGGGGGAAGATGGATAAATAATTCTGTACACGCTGCCCTGGCCTCTGGAGCTCAGCTGCCAGTCCAC
 GTCTAGGGAATCTTAGCATCTGGGACCAAGACACTTTACAGCAATCATCACCCCTTTCAGAGGAGGTGAGCTCAC
 CAGGACTCATCTGCCATTTTCAGACCTTTTGCTGCTACCTGCCAGGTGGCCCCCAGTCTGACGAGAGATGGTGGGA
 TCTCTCAGTCTCCCCGGAAGTCTTGAAGCCAGTATCGCTGACCAGCAGTCTTGTCTTCTCATGCACCTCCTCCT
 CTTTCAGCCTGGGGAGCCGAGCTCAGAGGTCAAGGTGCTAGGCCCTGAGTATCCCATCCTGGCCCTCGTCGGGGGA
 GGAGGTGGAGTTCCCGTGCCACCTATGGCCACAGCTGGATGCCAGCAAATGGAGATCCGCTGGTTCCGGAGTCA
 GACCTTCAATGTGGTACACCTGTACCAGGAGCAGCAGGAGCTCCCTGGCAGGCAGATGCCGGCGTTCCGGAAACAG
 GACCAAGTTGGTCAAGGACGACATCGCCTATGGCAGCGTGGTCCCTGCAGCTTCACAGCATCATCCCCTCTGACAA
 GGGCACATATGGCTGCCGCTTCCACTCCGACAACCTTCTCTGGCGAAGCTCTCTGGGAAGTGGAGGTAGCAGGGCT
 GGGCTCAGACCCCTCACCTCTCCCTTGAGGGCTTCAAGGAAGGAGGCATTCAGCTGAGGCTCAGATCCAGTGGCTG
 GTACCCCAAGCCTAAGGTTTCAAGTGGAGAGACACCAGGGACAGTGCCTGCCCTCCAGAGTTTGAAGCCATCGTCTG
 GGATGCCCAGGACCTGTTTCACTCTGGAAACATCTGTGGTGTGTCGAGCGGGAGCCCTCAGCAATGTGTCCGTCTC
 CATCCAGAATCTCCTCTTGAGCCAGAAGAAAGAGTTGGTGGTCCAGATAGCAGACGTGTTCGTACCCGGAGCCTC
 TGCCTGGAAGAGCGCGTTTCGTCCGACCCCTGCCGCTGCTGTGGTCCCTGCGCGCGCTGGCGCTGGGCGTCTCCG
 GAAGCAGCGGAGAAGCCGAGAAAAGCTGAGGAAGCAGCGCGGAGAAGAGACAAGAGAAACTCACTGCAGAGCTGGA
 AAAGCTTCAGACAGAGCTTGACTGGAGACGGGCTGAAGGCCAGGCTGAGTGGAGAGCAGCCCAAAAATATGCAGT
 GGATGTGACGCTGGACCCGGGCTCGGCGCACCCAGCCTGGAGGTGTGCGAGGATGGCAAGAGCGTGTCTTCCCG
 CGGGGCGCGCCAGGCCCCGGGCGCTGGCCACCCGAGCGGTTCTCGGAGCAGACGTGCGCGCTGAGCCTGGAGCG
 GTTCTCGCGCGGCGCCACTACTGGGAGGTGCACGTGGGCGCGCGCAGCGCGTGGTTCCTGGGCGCGCTGCCTGGC
 CGCGGTGCGCGCGCGGGGCTGCGCGCTGAGCCCTGCGCGCGGCTACTGGGTGCTGGGGCTGTGGAACGGCTG
 CGAGTACTTCTGCTTGGCCCCGACCCGCTCGCGCTCACCCCTGCGCGTGCCTCCCGCGCGCGCTGGGCGTCTCCT
 GGACTACGAGGCGGAGAGCTGTCTTCTTCAACGTGTCCGACGGCTCCACATCTTCACTTCCACGACACCTT
 CTCGGGCGCGCTCTGTGCGTACTTCAGGCCAGGGCCACGACGGCGGCGAACATCCGGATCCCCTGACCATCTG
 CCCGCTGCCGTTAGAGGGACGGGCGTCCCCGAAGAGAACGACAGTGACACCTGGCTACAGCCCTATGAGCCCGC
 GGACCCCGCCCTGGACTGGTGGTGAAGGCGCCCTCGTGGCCGCGGGACTGGCCCCGGGGGGCCCCCTGGATCCAG
 GCCAGCGCTTTGCTCTCCTGCTCCGTCTGAAGGGAGCAGGTGCACCAGCCAAAATGTGAGCGAGGGGGACAAAGA
 GAGGGACCTTTGCCTACGTAGATGTGTATGTGTAGTGGATTTTCAAGGAAAGGAGACAAGTCCAAAGCTCG
 TTTGTGGATTGTGGGACTGAGCGAAGGAGTACAAATATATCCACGTCGCTCAGAGCTGGGGTGTACAGGTGGGC
 GGTGGGCAAGAAGCCAGCATGGAAGAAAGAAGGGAGAAAACCTTTGGTGAAGTGCCTTAGAGGGATCAGTTAATTTG
 TATAGTTTTATATTTTTGTATATGTTTGCTAGCTCTAAAAAGGTGAGATGCAATAACACTTCGTAAGCAACGA
 GTTCACCTAAGTAAGGCTCAGATCCTAGTTTTAAAAACCATTTCCCATTAATAAGTGGAGGAACAGCTGCT
 TCTGAGCCGGGGCAAAAATTTCAAGGTGAGCCTGGAGCATTTGTGTGTGTGAAGTAAATAAAGGCTCAAAACGT
 GACGGCAACCCGGCAAAAGGTTAGGGAGCCAGGCCGAAGGGGCTCACTGACCAATTGTGGGACAATTTGAACAT
 CAGGATGAATAATGACAGGAGAGATTATAACACACTGAATAAAAAACATAATCCATGAGTTCATGCTGATACTCAA
 ATTTCTTTTTAAAAAGGAGAAAACAGGAAGGTTTCTTTGGAGGTGAAATCTAATTATTGGTGAGAGTCTTGAGA
 ACAGGCTGTTTCCAGTCTCAAAGCAGTAACCTTATACACTACTTATAAGTTTGAAGGGGAAAGGTTACCTTTAC
 AATGGAGACATCTACCAGATCATCCAAGTGATTAATTTAATCATCAATGATGGGACCAAGGACATTATAGT
 TTGACAACCTGGGGAAAGAAGTGTCTTCAACCCCTACCCCAAGACATTTCTCTGTGCGCCAGGCTGGAGTGCA
 GCCTCAACCTCCTGGGCCCAAGTGATCCTCCACCTCAGCACACAACACCATGCCCAATTTTAAGTGCCTTATAG
 AGACGGGGGTCTCACTTTGTTACCCAGGCTGGTCTCAAACTCCTGCGCTCAAGCAATCCTCCACCTGGGCTCC
 CAAAATGCTGGGTGTACAGGCATGAGCCGCTGTGCTGGCTTCATTTTCAGAGTGAGACATTTGTACTGTGGCTA
 TGTAGGAGAACATTTGTTCTTAGCAACATACTGAAGTTTTAGATATTAATTAACACAGTGTCTGCCACTGA
 ATTTCCAGTGACTAAGTGGAAAATATAAAACATATGAATATAAAGAAAAGAAAGAGACAAGTCAAATGTAGTAA
 ATGACAACACTTGGTGAAGTCTAGGTGAGTGGTGGACAGATGTTTATTGTACTATCAATGTGGCTTTGCTGTGGGT
 TTGAAATTTTGCAAACTAAGAGTTGGGTGGCGGGGAGAAAGATACACCAAAAACTAAGTGATTATCTTTGGATG
 GGAAAATGTTTGGTAATTCATTCTTAAATGTCTTCTTTGTATTTTTTAATGTTCAATAATGTATATGTATCAG
 TTCTGTAATAAAGGGGAAAACACTTTTCA

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FIGURE 124

MVDLSVSPDSLKPVSILTSSLVFLMHLLLLQPGEPSSEVKVLGPEYPILALVGEEVEFPCHLWP
QLDAQQMEIRWFRSQTFTNVVHLYQEQQELPGRQMPAFRNRTKLVKDDIAYGSVVLQLHSIIPS
DKGTYGCRFHSDNFSGEALWELEVAGLGSDPHLSLEGFKEGGIQLRLRSSGWYPKPKVQWRDH
QGQCLPPEFEAIVWDAQDLFSLETSSVVVRAGALSNVSVSIQNLLLSQKKELVVQIADVFPVGA
SAWKSAFVATLPLLLVLAALALGVLRKQRRSREKLRKQAEKRQEKLTAELEKLQTELDWRRAE
GQAEWRAAQKYAVDVTLDPASAHPSLEVSEDGKSVSSRGAPPGPAPGHPQRFSEQTCALSLE
FSAGRHYWEVHVGRRSRWFLGACLAAPRAGPARLSPAAGYWVLGLWNGCEYFVLAPHRVALT
LRVPFRRLGVFLDYEAGELSEFFNVSDGSHIFTFHDTFSGALCAYFRPRAHDGGEHPDPLTICP
LPVRGTGVPEENDSDTWLQPYEPADPALDWW

Important features of the protein:**Signal peptide:**

amino acids 1-34

Transmembrane domain:

amino acids 247-272

N-glycosylation sites.

amino acids 102-106, 139-143, 224-228, 464-468, 516-520

Tyrosine kinase phosphorylation site.

amino acids 105-114

N-myristoylation sites.

amino acids 129-135, 220-226, 399-405, 423-429, 480-486

Amidation site.

amino acids 390-394

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FIGURE 125

TATAGTCCCAGCTACTCATGGGGCTGATGCAGGTTGAGGCGAGGAGGTTTCATGAGCCCAGGAGGTTGGAGCTGTAA
TGAGCTAGGATTTCTGCCTCTGCACTCCTAGCTGGATGACAGAGCAAGACCCCTGTCTCAAAAAAGAAAAA
AAAAAGAATGCATGAACCAGACATGACAGTTCTGGCCTCAAAGATCTTCCAAAGGAAATGATTTTTTTTTTAAACC
ACCAATGCTGCAGGAAAAAGCAACATATTTAAGTTATCCAATAACACCTATCCAATAATTGTAATCATTATCAT
GACATGGTAGAGTTGTTTATATTTCTTTTCTTTTAGGTGAAACACCATTCAAAGTCGTAGTCAAATCTCTTTCA
CCTAAAGAGTTGGTCCGGATACATGTCCCTAAACCTTTGGACAGGAATGATGGAACATTTTTGATGAGATATAGG
ATGTATGAACTGTGATGAAGGCCTGAAGATAGAGGTCCTTTATGGTGATGAACATGTGGCTCAGTCTCCCTAT
ATTTTGAAGGACCAGTGTACCATGAGTACTGTGAGTGTCCGGAAGATCCTCAGGCCCTGGCAGAAGACTCTTTCT
TGTCACCAAGGAACCACAGATTGCAAAAGATTTTGTCTCCTTTCCAGCATCAATCTCCAGCAAATGCTAAAA
GAAGTCCCCAAAAGGTTTGGGGATGAGAGAGGTGCCATTGTTTATTACACGATTCTCAATAACCATGTTTACCGG
AGATCTTTAGGGAAATACACAGACTTCAAGATGTTCTCTGATGAGATTTTGTATCATTGACAAGAAAGGTCCTT
CTCCAGATTTAGAATTTTATGTTAATCTTGGAGATTGGCCCTTGGAGCATCGAAAAGTCAATGGAACCCCTAGC
CCCATACCTATCATTTCTGGTGTGGCTCTCTGGATTCAAGAGATGTTGTCTCTCAACGTATGACATCACCCAC
TCCATGCTTGAAGCCATGCGGGGTGTTACAAATGATCTCTCTCTATTCAGGGAAATACAGGGCCTTCTGGATC
AATAAACAGAGAGAGCTTTCTTTCAGAGGTAGAGACAGCCGAGAGGAGAGGCTCCAGTTGGTACAGCTGTCCAAA
GAAATCCTCAGCTACTAGATGCAGGAATTACAGGATATTTCTTTTTTCCAAGAGAAAAGAAAGGAGCTTGGAAA
GCCAAGTTGATGGGTTTCTTTGATTTCTTTAAGTACAAGTATCAAGTAAATGTGGATGGGACCGTGGCTGCTTAC
AGATATCCATATCTCATGCTGGGCGACAGTCTGGTTTTAAAGCAGGACTCGCCATATTATGAACATTTCTCATG
GCAC TAGAACCCTTGAAGCATTATGTTCCAAATTAAGAAATCTGAGTGATTTATTAGAGAAAGTTAAATGGGCT
AAGGAAAATGATGAAGAAGCCAAGAAGATTGCAAAAGAAGGACAGTTGATGGCTAGGGACCTACTACAGCCACAC
AGGCTTTACTGCTACTATTACCAAGTACTGCAGAAATATGCCGAGCGCCAGTCCAGCAAACCCGAAGTACGTGAT
GGAATGGAACCTTGTCTCAGCCAGAAGATAGCACAGCCATCTGCCAGTGCCACAGGAAAAGCCTTCAAGAGAA
GAACCTTGAAGTCAAGCCAGAAATCACACTCCTGTGTATCCCGGTACACTTTAAGGAAAGATTGAATCTAAGCTGT
GAAGGACAGTATAGAAGACTGCACCAAGTGGACTAGTTCTCCCGGTGGCTTTATATATGTAGATGGATATAGCAG
TACTGGTTGAGTATCCCTCATCTGAAATGCTTAGGACCAGGAGTGTTCAGGCTTCAGATTTTTTAAGATTTGGG
AATATTTGATGTACATAATGAGGTATCTTGGGGATGAGATCCAAGTCTAAACACAAAATTCATTTATATTTTAT
ATATACCTTGTTTACATACCCCTGAAGGTAATTTTATATAATTTTAAATAATTTGTGCATGAACAAAGTTTGT
ATACATTGAACCTGTAGAAAGCAAAGGTGTCACTACTTTAGCGCAAGTGGTGGTGTGTCAGCACTCAAAAGTT
TTGGATTTTGGGGTATTTTCAAGATTTTGTATGAGGAATGTTCAACCTGTATTTGAACAAGCATTACCA
AATATCATTGAATATTAATATCTTTTGGCTAAAACTGCTATTATCAGCATCATAGTTTCTCTAAAAAGAAAAT
TGGGGATCATAGCCGATAGAGAGACTTGCTAAAAATATAAATCAGCCTCTGCAAACTGTTTACATATTTATGGT
TTACATATTTTATTTGGTTTATTTCTATCCCTGTTCACCTTTTCTCTTCCACTTCCAATTATGAAGAGAAAATAT
TTGTTTCAAGGTTGTCCCCCGCCCCCGCTCACTGCATAATTTCTCCTCTTACAAGCTGCTTTTGGCTTTTATTAA
TAACAGCTTCTCTTTAGAAAGGTCTGATAAGGATATTTAAGGAAGAAGAGAAATGACTCTGTATTTAAAGGTGGCAT
GGAGACTGTGGAGGGAATATTTTTTAAAGCACTACTCATATCTCTTAAACTAAATTTTGGCAAAGCCCGAGACAA
CATTAAGGAGGAATGTACCTTAAGTTAGTAATTTCCAAATCTATCTGACTTGTATACCATCAAGACAAATACAG
TTATTAACATAGATGAAGGTATGCTATAGGCATCATTATTATCTCTATATTGAATAGGTGAAAGATAACTGTAG
TCAGGTGAAAGGCATTTCATCATTTTTTAAGCTGAAAAGGGGATCCTTGAAAACACTGAAAACCTCTACAACAATCT
TCAGGAAGCCTGCTATCTTGGGATTCACTAATAATAGGCCAAGAACAAGGCAAGCATCCATTCTCTCACTCCACC
ACTTTTCTATTTTCACTGGGTGTCTTGGTACGATGAAGACTTTGGAAATTTCTCTCTTTTAGGACAGGGTCA
GGATTTAGGACTCATAGCCTGAAAGCTCATTACATACTCCTTGTAACCATCAGTCCAAGGTTTCACTTCACTAAAG
TGCATGTTCTAAACAAGAGCTATCCTCATTCCAAATTTTAAATATGTACTCTGGCCGGTTGCAGTGGCTCACG
CCTGTAATCCAGCACTTTGGCAGGCGGAGATGGGCGGATCTTTTGAAGTCAAGGATTTGAGACCAGCCTGGCCA
ACATGGTGAACCCCGTCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGCATTTGCCTGTAATCCAGCT
ACTCGGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTACACCCTG
CAC'TCCAGCT'GGGTGACAGAGTGAGACTCCATCTCAAAAATGAAAATAAAAAATATGTATTTCTCTTAA
CTGAAATATTTACTTAACTCTGGAAAACAATGTAACATTTTTTAAAGTGTTTACATCTATTCTTGTCTGAAGAACA
TAAACAGAATTTTTTGAATAAGCATAACCAATTTTCAAGACAGTCTAATCAATGCCAAGTATCCAAGGCAAACTC
TAATACCCATCCATTGTGCAAAACCACAAGCAGCAAGTATTAAATAAGAGCAAGCTGTCTGAGCCCATACCTA
ATGAATTTGTGTCTTAAATATTTGTACATTTGTGTTTGAAGCTTGTCAAAACTGGGATTATGGCAAGAAAGGTTGCC
TAACTCATACCTTTCTGCCTCAAATTCAGGTGCTAAAGGCTAATGGCATTTTAAACATCTTACATTTTTAAAAA
TTTATATTTGCCTCTGCCAAACAGGCCTAATAGTTAAAAGCAAGTTGAGACAAACCAGGCAGATTCACTGTGTGGA
ACAGGAAGGATGTGCTTTAAAAAAGGTGGAATCCCTCAAAAAATCTTATAGGGAGACAGCCCTAATCTACA
TAATTTCTTCACTCTGCCAATTCAGCCGAGCCTTTAAAGAGTTAGTGTTAATGGCTTTTGGTTTGAAGCAAAA
ATGCATCTATGTGGTTGAAAGTTTGGGAGGAGATTACCAATATCTGAGGAGAAGATGGAGTGAAGGGAATTTCTT
ACTTTTTGCTTTTATACCTTTCTATAATATTTAGATTTTTTTTTTACTGTAAGTATGGATCAAAATGCAAAATAAG
AAAAATGCCAACCTTAGAAAAGACAATAAATGCACAAAAGATATAAACAGGAACAGCAAAATATTTATTTTTTC
CATTTTGCTCTTTTTAAATCTATGTTTAGAACCTTTATATCTTGGGACTTATGTATATATATACCTTTTAAATAAA
ATAAATTTTCTAAATAAAAAGTTG

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FIGURE 126

MVELFIFLFLLLGETPFFKVVKSLSPKELVRIHVPKPLDRNDGTFLMRYRMYETVDEGLKIEVL
YGDEHVAQSPYILKGPVYHEYCECPEDPQAWQKTLSCPTKEPQIAKDFASFPSINLQQMLKEV
PKRFGDERGAIVHYTILNNHVYRRSLGKYTDEKMFSD EILLSLTRKVLLPDLEFYVNLGDWPL
EHRKVNGTPSPIPIISWCGSLDSRDVVLPTYDITHSMLEAMRGVTNDLLSIQGNTGPSWINKT
ERAFRGRDSREERLQLVQLSKENPQLLDAGITGYFFFQEKELGKAKLMGFFDFFKYKYQV
NVDGTVAAYRYPYMLGDSLVLKQDSPYEHFYMALEPWKHYVPIKRNLSDLLEKVKWAKEND
EEAKKIAKEGQLMARDLLQPHRLYCYYYQVLQKYAERQSSKPEVRDGMELVPQPEDSTAICQC
HRKKPSREEL

Important features of the protein:**Signal peptide:**

amino acids 1-16

N-glycosylation sites.

amino acids 250-254, 363-367

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 444-448

N-myristoylation site.

amino acids 208-214, 319-325, 388-394

Endoplasmic reticulum targeting sequence.

amino acids 448-453

Mitochondrial energy transfer proteins signature.

amino acids 25-34

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FIGURE 127

AGCCGTCGGAGGGAGCCGGAGCGCTTCTCCCGAGTTGGTGATAGATTGGTGGTTCATCCAACAT
GCAGAAATGAATGAGCAGTGAAAAGCAGCAGAGCCGATGGGTCATGAGGATGTAAGTGCGTTT
GAAGGCTTCCACACCCTCTACTCCAGGAATCATGAATAAACTGGAGGATAAGCAGGACCAGAT
GATACCAATGAAGAGAAGTTTACAGGGCCCTCTATTGCCAACTGTTAAGTTTCCTGCTGATCTTG
GCACTGACCGAAGCGCTGGCATTTCGCATCCAGGAACCATCTCCCAGGGAATCTCTTCAGGTC
CTCCCTTCAGGCACTCCCCCGGGAACCATGGTGACAGCACCCACAGCTCTACCAGACATACT
TCTGTGGTGATGCTGACCCCCAATCCCGATGGACCCCCCTCACAGGCTGCAGCTCCCATGGCA
ACACTGACACCCCCGTGCAGAGGGGCACCCCTCCTACGCACACCATCTCCACCATCGCTGCGACA
GTAACCGCCCCCTATTCTGAAAGCTCCCTGTCCACAGGGCCCGCTCCAGCAGCCATGGCAACC
ACATCCTCCAAGCCAGAGGGCCGCCCTCGAGGGCAGGCTGCCCCACCATCCTGCTGACAAAG
CCACCGGGGGCCACCAGCCGCCACCACAGCGCCCCCGCACTACCACACGCAGGCCCCCC
AGGCCCCCAGGCTCTTCCCGAAAAGGGGCTGGTAATTCATCACGCCCTGTCCCGCTGCACCT
GGTGGCCACTCCAGGAGTAAAGAAGGACAGCGAGGACGAAATCCAAGCTCCACACCTCTGGGG
CAGAAGCGGCCCTGGGGAAAATCTTTCAGATCTACAAGGGCAACTTCACAGGGTCTGTGGAA
CCAGAGCCCTCTACCCTCACCCCCAGGACCCCACTCTGGGGCTACTCCTCTTCACCACAGCCC
CAGACAGTGGCTGCGACCACAGTGCCCAGCAATACCTCATGGGCACCCACCACCACCTCCCTG
GGGCTGCAAAGGACAAGCCAGGCCCTTCGCAGAGCAGCCCAGGGGGGTGGTTCTACCTTCACC
AGCCAAGGAGGGACACCAGATGCCACAGCAGCCTCAGGTGCCCTGTGAGTCCACAAGCTGCC
CCAGTGCCCTTCTCAGCGCCCCCACCACGGTGACCCACAGGATGGCCCCAGCCATAGTGACTCT
TGGCTTACTGTTACCCCTGGCACCAGCAGACCTCTGTCTACCAGCTCTGGGGTCTTCACGGCT
GCCACGGGGCCCACCCCAGCTGCCTTCGATACCAGTGTCTCAGCCCCTTCCCAGGGGATTCTT
CAGGGAGCATCCACAACCCCAACAAGCTCCAACCCATCCCTCCAGGGTCTCAGAAAGCACTATT
TCTGGAGCCAAGGAGGAGACTGTGGCCACCCTCACCATGACCGACCGGTGCCAGTCCTCTC
TCCACAGTGGTATCCACAGCCACAGGCAATTTCTCAACCGCTGGTCCCCGCCGGGACCTGG
AAGCCTGGGACAGCAGGGAACATCTCCCATGTGGCCGAGGGGGACAAACCGCAGCACAGAGCC
ACCATCTGCCTGAGCAAGATGGATATCGCCTGGGTGATCCTGGCCATCAGCGTGCCCATCTCC
TCCTGCTCTGTCTGCTGACGGTGTGCTGCATGAAGAGGAAGAAGAAGACCGCCAACCCGGAG
AACAACCTGAGCTACTGGAACAACACCATCACCATGGACTACTTCAACAGGCATGCTGTGGAG
CTGCCCAGGGAGATCCAGTCCCTTGAAACCTCTGAGGACCAGCTCTCAGAGCCCCGCTCCCCA
GCCAATGGCGACTATAGAGACACTGGGATGGTCCTTGTTAACCCCTTCTGTCAAGAAACACTG
TTTGTGGGAAACGATCAAGTATCTGAGATCTAACTACAGCAGGCATCACTTTGCCATTCCGTA
TTTTTCGTCTCTAAATTATAAATATACAAATATATATATTATAAATATAACCTTGTGTAAACC
TGACTTAATGAGAAACATTTTCAGCTTTTTTTCCTATGAATTGTCAACATCTTTTTTACAAGT
GTGGTTTAAAAAAAAAAAAAAGCTTTACAGAATGATCTGTGGCTTTATAAAATAAAGGTATTTCT
AAGCAAAAAAAAAAAAAAAAAA

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FIGURE 128

MKRSIQALYCQLLSFLLILALTEALAFAIQEPPRESLQVLPSGTPPGTMVTAPHSSSTRHTSV
VMLTFNPDGPPSQAAAPMATLTPRAEGHPPTHISTIAATVTAPYSESSLSTGPAPAAMATTS
SKPEGRPRGQAAPTILLTKPPGATSRPTTAPPRTTTRRPPRPPGSSSRKGAGNSSRPVPPAPGG
HSRSKEGQRGRNPSSTPLGQKRPLGKIFQIYKGNFTGSVEPEPSTLTPRTLWGYSSSPQPQT
VAATTVPSTNTSWAPTTTSLGPAKDKPGLRRAAQGGGSTFTSQGGTPDATAASGAPVSPQAAPV
PSQRPHHGDPQDGPSHSDSWLTVTPGTSRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGI PQG
ASTTPQAPTHPSRVSESTISGAKEETVATLTMTRVPSPLSTVVSTATGNFNLRLVPAGTWKF
GTAGNISHVAEGDKPQHRATICLSKMDIAWVILAISVPISSCSVLLTVCCMKRKKKTANPENN
LSYWNNTITMDYFNRHAVELPREIQSLETSEDQLSEPRSPANGDYRDTGMVLVNPFQETLFV
GNDQVSEI

Important features of the protein:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 469-487

N-glycosylation sites.

amino acids 178-182, 223-227, 261-265, 446-450, 504-508, 509-513

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 495-499

N-myristoylation sites.amino acids 44-50, 48-54, 175-181, 222-228, 279-285, 286-292,
288-294, 296-302, 351-357, 374-380, 427-433, 442-448**TonB-dependent receptor proteins signature 1.**

amino acids 1-44

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FIGURE 129

AGGCGAGGCGCGGCGCCGCTGCACACACGCACACGGAGCT**ATG**GGGTGCCATGTTGCCACCAG
CTGCCACGTGGCCTGGCTTTTGGTGCTGATCTCTGGATGCTGGGGCCAGGTGAACCGGCTGCC
CTTCTTCACCAACCACTTCTTTGATACATACCTGCTGATCAGCGAGGACACGCCTGTGGGTTC
TTCTGTGACCCAGTTGCTGGCCCAAGACATGGACAATGACCCCCTGGTGTGTTGGCGTGTCTGG
GGAGGAGGCCTCTCGCTTCTTTGCAGTGGAGCCTGACACTGGCGTGGTGTGGCTCCGGCAGCC
ACTGGACAGAGAGACCAAGTCAGAGTTCACCGTGGAGTTCTCTGTGACGCGACCACCAGGGGGT
GATCACACGGAAGGTGAACATCCAGGTCGGGGATGTGAATGACAACGCGCCACATTTACAA
TCAGCCCTACAGCGTCCGCATCCCTGAGAATACACCAGTGGGGACGCCCATCTTCATCGTGAA
TGCCACAGACCCCGACTTGGGGGACAGGGGGCAGCGTCCTCTACTCCTTCCAGCCCCCTCCCA
ATTCTTCGCCATTGACAGCGCCCGCGGTATCGTCACAGTGATCCGGGAGCTGGACTACGAGAC
CACACAGGCCCTACCAGCTCACGGTCAACGCCACAGATCAAGACAAGACCAGGCCTCTGTCCAC
CCTGGCCAACCTTGGCCATCATCATCACAGATGTCCAGGACATGGACCCCATCTTCATCAACCT
GCCTTACAGCACCAACATCTACGAGCATTCTCCTCCGGGCACGACGGTGCGCATCATCACCGC
CATAGACCAGGATAAAGGACGTCCCCGGGGCATTTGGCTACACCATCGTTTCAGGGAATACCAA
CAGCATCTTTGCCCTGGACTACATCAGCGGAGTGCTGACCTTGAATGGCCTGCTGGACCGGGA
GAACCCCTGTACAGCCATGGCTTCATCCTGACTGTGAAGGGCACGGAGCTGAACGATGACCG
CACCCCATCTGACGCTACAGTCACCACGACCTTCAATATCCTGGTTATTGACATCAATGACAA
TGCCCCGGAGTTCAACAGCTCCGAGTACAGCGTGGCCATCACTGAGCTGGCACAGGTCGGCTT
TGCCCTTCCACTCTTCATCCAGGTGGTGGACAAGGATGAGAATTTGGGCCTGAACAGCATGTT
TGAGGTGTACTTGGTGGGGAACAACTCCCACCACTTCATCATCTCCCCGACCTCCGTCCAGGG
GAAGGCGGACATTTCGTATTCGGGTGGCCATCCCCTGGACTACGAGACCGTGGACCGCTACGA
CTTTGATCTCTTTGCCAATGAGAGTGTGCCTGACCATGTGGGCTATGCCAAGGTGAAGATCAC
TCTCATCAATGAAAATGACAACCGGCCCATCTTCAGCCAGCCACTGTACAACATCAGCCTGTA
CGAGAACGTCACCGTGGGGACCTCTGTGCTGACAGTCCTGGTGAGTCCCCGCTTCACTGCAGG
GCCACTGAGCTCTCCAGGGCCGACTGTGGTGAGGCACCCAGAGGGATTTTGTCCAAGGGACCT
CAGCAATCAGGGAAGGAGGCACCCCCAAATCCCTGAGCTGTGTTTGTGTTGGTGTAT**TAA**ATAAA
GTTTTTGGACTCTTCAGGAAGGGGCTCCCTTGACCTAGGTTGCAATATGGAAAAGGAGCCAAC
CTGAGGGGTGACGAGACTGAGCTGAGGACACTGGTTTTTCTGCCCTTCCCTGAGAGAGACTCAG
TGAGGGTGGGCTGGGAGCCCTGGAAGCCCCCTCAATGGGTGGGAAGGTGCCAGCCATCCTTG
AGAAGGGCAACCTCTCCATGTGAGCAGAGCCAGAGAGGGGCAGGCGCCTGGAGGGTACC
GGGACACCCCAAGCTGCCCATGGCTGGACTTGCCCTTGACAAGGGGCCCTCCAGTGTCATT
TGTATCTGTCAGTACTCTTGGTTGCAAGGGACAGAAACCCTTAAGTAGTTCAAGCAAAAAGG
ATTGGCTCATGTAACCAAAAGTATAAGTGATTCAGGCCGGGCTCGGTGGCTCACGCCTGTC
ATCCAACACCTTGAGAAAGCCGAGGTGGGCGGATCACTTGAGGTGCGGAGTTTGAGACCAGCC
TGGCCAACATGGCAAAACCCCGTCTCTACTAAAAATACAAAATTAGCCGGGTGTGGTGGCAC
ACGCCTGTAGTCCCAGCTACTAGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGCGG
AGGTTGCAGTGAGCCGAGATTGTGTCACTGCCCTCCAGCCTGGGCGACAGAGCCAGATTCTGT
CTC

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FIGURE 130

MGCHVATSCHVAWLLVLISGCWGQVNRLPFFTNHFFDTYLLISEDTPVGSSVTQLLAQDMDND
PLVFGVSGEEASRFFAVEPDTGVVWLRQPLDRETKSEFTVEFSVSDHQGVITRKVNIQVGDVN
DNAPT FHNQPYSVRIPENTPVGTPIFIVNATDPDLGAGGSVLYSEQPPSQFFAIDSARGIVTV
IRELDYETTQAYQLTVNATDQDKTRPLSTLANLAIITDVQDMDPIFINLPYSTNIYEHSPPG
TTVRIITAIQDKGRPRGIGYTIVSGNTNSIFALDYISGVLTNLGLLDRENPLYSHGFILTVK
GTELNDDRTPSDATVTTTFNILVIDINDNAPEFNSSEYSVAITELAQVGFALPLFIQVVDKDE
NLGLNSMFEVYLVGNNSHHFIISPTSVQKGADIRIRVAIPLDYETVDRYDFDLFANESVPDHV
GYAKVKITLINENDNRPIFSQPLYNISLYENVTVGTSVLTVLVSPRFTAGPLSSPGPTVVRHP
EGFCPRDLSNQGRRHPQIPELCLLVY

Important features of the protein:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 355-374

N-glycosylation sites.amino acids 155-159, 206-210, 349-353, 393-397, 434-438, 466-470,
472-476**N-myristoylation sites.**

amino acids 2-8, 49-55, 162-168, 270-276, 278-284, 316-322

Amidation site.

amino acids 515-519

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

Leucine zipper pattern.

amino acids 298-320

PTS HPR component serine phosphorylation site signature.

amino acids 377-393

Cadherins extracellular repeated domain signature.

amino acids 120-131, 336-347

Cadherins extracellular

amino acids 120-144, 336-360

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FIGURE 131

GTGGGCCGCCCCCTGCTGCTGCCGTCC**ATG**CTGATGTTTGCGGTGATCGTGGCCTCCAGCGGGC
TGCTGCTCATGATCGAGCGGGGCATCCTGGCCGAGATGAAGCCCCTGCCCCTGACCCGCCCG
GCCGCGAGGGCACAGCCTGGCGCGGGAAAGCCCCCAAGCCTGGGGGCCTGTCCCTCAGGGCTG
GGGACGCGGACTTGCAAGTGCGGCAGGACGTCCGGAACAGGACCCTGCGGGCGGTGTGCGGAC
AGCCAGGCATGCCCCGGGACCCCTGGGACTTGCCGGTGGGGCAGCGGCGCACCCCTGCTGCGCC
ACATCCTCGTAAGTGACCGTTACCGCTTCCTCTACTGCTACGTCCCCAAGGTGGCCTGCTCTA
ACTGGAAGCGGGTGATGAAGGTGCTGGCAGGCGTCTGGACAGCGTGGACGTCCGCCTCAAGA
TGGACCACCGCAGTGACCTGGTGTTCTGGCCGACCTGCGGCCTGAGGAGATTTCGCTACCGCC
TGCAGCACTACTTTAAGTTCCTGTTTGTGCGGGAGCCCTTGGAACGCCTCCTCTCTGCCTACC
GCAACAAGTTTGGCGAGATCCGAGAGTACCAGCAACGCTATGGGGCTGAGATAGTGAGGCGGT
ACAGGGCTGGAGCGGGGCCAGCCCTGCAGGCGACGATGTCACATTCCCCGAGTTCCTGAGAT
ACCTGGTGGATGAGGACCCTGAGCGCATGAATGAGCATTTGGATGCCCGTGTACCACCTGTGCC
AGCCTTGTGCCGTGCACTATGACTTTGTGGGCTCCTATGAGAGGCTGGAGGCTGATGCAAATC
AGGTGCTGGAGTGGGTACGGGCACCACCTCACGTCCGATTTCCAGCTCGCCAGGCCCTGGTACC
GGCCAGCCAGCCCCGAAAGCCTGCATTACCACTTGTGCAGTGCCCCCGGGCCCTGCTGCAGG
ATGTGCTGCCTAAGTATATCCTGGACTTCTCCCTCTTTGCCTACCCACTGCCTAATGTCACCA
AGGAGGCGTGTCAGCAG**TGAC**CATGGGTGTGGGGCCAGCAGCTGGTGGGGACTGGTTTCAACG
CCAGCTTTCTGTGCTTCTGCCTGTCATTTCGGAGAACTCTGGCTCTGGGGCTTGGGGCTTCTC
AGGATCCTGGATGGCAGAGACTGCCCTCAGAAGTTCCTTGTCCAGGGTGGGCACCCACAGTGA
CTCAGAGGACAGGGCTAGGCAGGAGACCTGCTGCTCCTCATTGGGGGGATCTCTTGGGGGGCA
GACACCAGTTTGCCAATGAAGCAACACATCTGATCTAAAGACTGGCTCCAGACCCCGGGCTGC
CAGGATTATGCAGTCCACTTGGTCTACCTTAATTTAACCTGTGGCCAAACTCAGAGATGGTAC
CAGCCAGGGGCAAGCATGACCAGAGCCAGGGACCCTGTGGCTCTGATCCCCCATTTATCCACC
CCATGTGCCTCAGGACTAGAGTGAGCAATCATACCTTATAAATGACTTTTGTGCCTTTCTGCT
CCAGTCTCAAAATTTCTACACCTGCCAGTTCTTTACATTTTCCAAGGAAAGGAAAACGGAA
GCAGGGTTCTTGCTGGTAGCTCCAGGACCCAGCTCTGCAGGCACCCAAAGACCCTCTGTGCC
CAGCCTCTTCCTTGAGTTCTCGGAACCTCCTCCCTAATTCTCCCTTCCTTCCCCACAAGGCCT
TTGAGGTTGTGACTGTGGCTGGTATATCTGGCTGCCATTTTTCTGATGCATTTATTTAAAT
TGTACTTTTTGATAGAACCCTTGTAAGGGCTTTGTTTTCTAATAGCTGACTTTTTAATAAAG
CAGTTTTATATAT

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FIGURE 132

MLMFAVIVASSGLLLMIERGILAEWKPLPLHPPGREGTAWRGKAPKPGGLSLRAGDADLQVRQ
DVRNRTLRAVCGQPGMPRDPWDLFVGQRRTLLRHILVSDRYRFLYCYVPKVACSNWKRVMKVL
AGVLDSVDVRLKMDHRSDLVFLADLRPEEIIRYRLQHYFKFLFVREPLERLLSAYRNKFGEIRE
YQQRYGAEIVRRYRAGAGPSPAGDDVTFPEFLRYLVDEDPERMNEHWMPVYHLCQPCAVHYDF
VGSYERLEADANQVLEWVRAPPHVRFPARQAWYRPASPESLHYHLCAPRALLQDVLPKYILD
FSLFAYPLPNVTKEACQQ

Important features of the protein:

Signal peptide:

amino acids 1-23

N-glycosylation sites.

amino acids 67-71, 325-329

Tyrosine kinase phosphorylation sites.

amino acids 152-159, 183-183

N-myristoylation sites.

amino acids 89-95, 128-134

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FIGURE 133

CGGCAGTTCTGGCCCCTGCAGCTGGAGGTACCCTGAGTTCTGAGGGTCGTAGTGCTGTTTCTG
GTATTCTCATCGCGGTACCTCTACCGGTGTGGACAAGTAAAGTTTGAATCAGCTTCTCCATG
GCCTGGGCACCAGTTCCCGGCTGAGCCATTTTCCTTTTGGCTAAAAGTCCCCGCCCAGAGGCC
AATTCGTCGCGGCGGCGGTGGAGATCGCAGGTCGCTCAGGCTTGCAGATGGGTCAAGGGTTGT
GGAGAGTGGTCAGAAACCAGCAGCTGCAACAAGAAGGCTACAGTGAGCAAGGCTACCTCACCA
GAGAGCAGAGCAGGAGAATGGATGCGAGCAACATTTCTAACACCAATCATCGTAAACAAGTCC
AAGGAGGCATTGACATATATCATCTTTTGAAGGCAAGGAAATCGAAAGAACAGGAAGGATTCA
TTAATTTGGAAATGTTGCCTCCTGAGCTAAGCTTTACCATCTTGTCTACCTGAATGCAACTG
ACCTTTGCTTGGCTTCATGTGTTTGGCAGGACCTTGCGAATGATGAACTTCTCTGGCAAGGGT
TGTGCAAATCCACTTGGGGTCACTGTTCCATATACAATAAGAACCCACCTTTAGGATTTTCTT
TTAGAAAATTGTATATGCAGCTGGATGAAGGCAGCCTCACCTTTAATGCCAACCAGATGAGG
GAGTGAACACTTTATGTCCAAGGGTATCCTGGATGATTCGCCAAAGGAAATAGCAAAGTTTA
TCTTCTGTACAAGAACTAAATTGGAAAAAACTGAGAATCTATCTTGATGAAAGGAGAGATG
TCTTGGATGACCTTGTAACATTGCATAATTTTAGAAATCAGTTCTTGCCAAATGCACTGAGAG
AATTTTTTCGTCATATCCATGCCCCCTGAAGAGCGTGGAGAGTATCTTGAAACTCTTATAACAA
AGTTCTCACATAGATTCTGTGCTTGCAACCCTGATTTAATGCGAGAACTTGGCCTTAGTCCTG
ATGCTGTCTATGTACTGTGCTACTCTTTGATTCTACTTTCCATTGACCTCACTAGCCCTCATG
TGAAGAATAAAATGTCAAAAAGGGAATTTATTCGAAATACCCGTCGCGCTGCTCAAAATATTA
GTGAAGATTTTGTAGGGCATCTTTATGACAATATCTACCTTATTGGCCATGTGGCTGCATTAAA
AAGCACAATTGCTAGGACTTCAGTTTTTACTTCAGACTAAAGCTACCCAAGGACTTAGCAGAT
ATGGGGGTACATCAGTGCTGGTCATTGTAGCCTGAGTATACAATCAAGCTTCAGTGTGCAAC
CTTTTTTCTTTTGCCATTTTCTATTTTAGTAATTTCTTGGGGAATAAATAATTTTGCAGA
ATTTTTCTTAATTTTGTATTATCACGTTTTGCACAAAGCAGAGCCACTGTCTAACACAGCTGTT
AACGAATGATAAACTGACATTATACTCTAAAAGATGGTGTATTTGTGCATTAGATTTGCCTGA
AAAACCTTTATCCATTTCCATTCCTTATACAAATACCATGTAATGTGTACATATTTAACTAAAG
AGATTTATAGTCATAATTATTTTATTGTAAAGATTTTAACTAAAGTTTTTCCTTTTCTCTC

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FIGURE 134

MGQGLWRVVRNQQLQQEGYSEQGYLTREQSRMDASNISNTNHRKQVQGGIDIYHLLKARKSK
EQEGFINLEMLPPELSFTILSYLNATDLCLASCWQDLANDELLWQGLCKSTWGHCSIYNKNP
PLGFSFRKLYMQLDEGSLTFNANPDEGVNYFMSKGILDDSPKEIAKFIFCTRTLNWKKLRIYL
DERRDVLDLVTLHNFRNQFLPNALREFFRHHAPEERGEYLETLITKFSHRFCACNPDLNRE
LGLSPDAVYVLCYSLILLSIDLTSPHVKNKMSKREFIRNTRRAAQNISDFVGHLYDNIYLG
HVAA

Important features of the protein:

Transmembrane domain:

amino acids 253-272

N-glycosylation sites.

amino acids 37-41, 87-91, 298-302

N-myristoylation site.

amino acids 110-116

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FIGURE 135

GGCACGAGGGAGCCTCCGTTAGGGGGTGGGAAAGGACTTTGCCATAGGTCGCTGAGGCCACCA
TCTGCTCTCTTACTGGCCAAGGGCGTAAAAAGATAGTCTTCCCATTAGCTAGAGAGCAAACCC
CAGAAAGCCTATTGGCTGCGCCGTCCGCGGGCCTTGGTCCGCTTTGAAGGCGGGCTGCGGCTG
CGAGAGGAGGGCGGGCGGGAGGCTAGCTGTTGTCGTGGTTGCTCGGAGGCACGTGTGCAGTCC
CGGAAGCGGCGAGGGGAAACTGCTCCGCGCGCGCCCGGGAGGAGGAACCGCCCGGTCTTTA
GGGTCCGGGCCCCGGCCGGGCCATGGATTCAATGCCTGAGCCCGCGTCCCGCTGTCTTCTGCTT
CTTCCCTTGCTGCTGCTGCTGCTGCTGCTGCTGCCGGCCCCGGAGCTGGGCCCCGAGCCAGGCC
GGAGCTGAGGAGAACGACTGGGTTCGCCTGCCCAGCAAATGCGAAGTGTGTAAATATGTTGCT
GTGGAGCTGAAGTCAGCCTTTGAGGAAACCGGCAAGACCAAGGAGGTGATTGGCACGGGCTAT
GGCATCCTGGACCAGAAGGCCTCTGGAGTCAAATACACCAAGTCGGACTTGCGGTTAATCGAA
GTCACTGAGACCATTTGCAAGAGGCTCCTGGATTATAGCCTGCACAAGGAGAGGACCGGCAGC
AATCGATTTGCCAAGGGCATGTCAGAGACCTTTGAGACATTACACAACCTGGTACACAAAGGG
GTCAAGGTGGTGATGGACATCCCCTATGAGCTGTGGAACGAGACTTCTGCAGAGGTGGCTGAC
CTCAAGAAGCAGTGTGATGTGCTGGTGGAAGAGTTTGAGGAGGTGATCGAGGACTGGTACAGG
AACCACCAGGAGGAAGACCTGACTGAATTCCCTCTGCGCCAACCACGTGCTGAAGGGAAAAGAC
ACCAGTTGCCTGGCAGAGCAGTGGTCCGGCAAGAAGGGAGACACAGCTGCCCTGGGAGGGAAG
AAGTCCAAGAAGAAGAGCAGCAGGGCCAAGGCAGCAGGCGGCAGGAGTAGCAGCAGCAAACAA
AGGAAGGAGCTGGGTGGCCTTGAGGGAGACCCCAGCCCCGAGGAGGATGAGGGCATCCAGAAG
GCATCCCCCTCTCACACACAGCCCCCTGATGAGCTCTTGAGCCCCACCCAGCATCCTCTGTCTTG
AGACCCCTGATTTTGAAGCTGAGGAGTCAGGGGCATGGCTCTGGCAGGCCGGGATGGCCCCGC
AGCCTTCAGCCCCCTCCTTGCCCTGGCTGTGCCCTCTTCTGCCAAGGAAAGACACAAGCCCCAG
GAAGAACTCAGAGCCGTCATGGGTAGCCACGCGTCCTTTCCCTCCCCAAGTGTTTCTCTC
CTGACCCAGGGTTCAGGCAGGCCTTGTGGTTTCAGGACTGCAAGGACTCCAGTGTGAACTCAG
GAGGGGCAGGTGTCAGAACTGGGCACCAGGACTGGAGCCCCCTCCGGAGACCAAACCTCACCAT
CCCTCAGTCCTCCCCAACAGGGTACTAGGACTGCAGCCCCCTGTAGCTCCTCTCTGCTTACCC
CTCCTGTGGACACCTTGCACTCTGCCTGGCCCTTCCCAGAGCCCAAAGAGTAAAAATGTTCTG
GTTCTGATTTCTGAAAAAAAAAAAAAAAAAAATTCCT

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FIGURE 136

MDSMPEPASRCLLLLPLLLLLLLLLLPAPELGPSQAGAEENDWVRLPSKCEVCKYVAVELKSAF
EETGKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTETICKRLLDYSLHKERTGSGNRFAKGM
SETFETLHNLVHKGVKVVM DIPYELWNETS AEVADLKKQCDVLVEEFEEVIEDWYRNHQEEDL
TEFLCANHVLKGGKDTSC LAEQWSGKKGDTAALGGKKSKKKSSRAKAAGGRSSSSSKQRKELGGL
EGDPSPEEDEGIQKASPLTHSPPEL

Important features of the protein:**Signal peptide:**

amino acids 1-26

N-glycosylation site.

amino acids 153-157

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 227-231, 228-232

Tyrosine kinase phosphorylation site.

amino acids 142-150

N-myristoylation sites.amino acids 36-42, 74-80, 86-92, 125-131, 222-228, 237-243,
250-256, 263-269**Amidation sites.**

amino acids 212-216, 222-226

ATP/GTP-binding site motif A (P-loop).

amino acids 62-70

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FIGURE 137

CACGCCTCCCGCTGCCAGCCCGGCACCGGGATCTTAATCAGTCACTATGAAAACCTCATTAGCT
CCACAGCA**ATG**AGTCCTCCACTGCTGAAGCTTGGCGCTGTGCTTAGTACCATGGCAATGATCT
CAAACCTGGATGTCCCAAACCTCTCCCATCCTTGGTGGGACTGAACACCACGAGGCTGTCGACTC
CGGATACCTTAACTCAGATTAGTCCTAAAGAAGGGTGGCAGGTGTACAGCTCAGCTCAGGATC
CTGATGGGCGGTGCATTTGCACAGTTGTTGCTCCAGAACAAAACCTGTGTTCCCGGGATGCCA
AAAGCAGGCAACTTCGCCAACTACTGGAAAAGGTTTCAAGACATGTCCCAGTCTATTGAAGTCT
TAAACTTGAGAACTCAGAGAGATTTCCAATATGTTTTTAAAAATGGAAACCCAAATGAAAGGGC
TGAAGGCAAAATTTTCGGCAGATTGAAGATGATCGAAAGACACTTATGACCAAGCATTTCAGG
AGTTGAAAGAGAAAATGGACGAGCTCCTGCCTTTGATCCCCGTGCTGGAACAGTACAAAACAG
ATGCTAAGTTAATCACCCAGTTCAAGGAGGAAATAAGGAATCTGTCTGCTGTCCTCACTGGTA
TTCAGGAGGAAATTGGTGCCTATGACTACGAGGAACTACACCAAAGAGTGCTGAGCTTGGAAA
CAAGACTTCGTGACTGCATGAAAAAGCTAACATGTGGCAAACCTGATGAAAATCACAGGCCCAG
TTACAGTCAAGACATCTGGAACCCGATTTGGTGCTTGGATGACAGACCCTTTAGCATCTGAGA
AAAACAACAGAGTCTGGTACATGGACAGTTATACTAACAATAAAATTGTTTCGTGAATACAAAT
CAATTGCAGACTTTGTGCTAGTGGGGCTGAATCAAGGACATAACAACCTTCCTTTCAAGTGGGCAG
GAACTAACCATGTTGTCTACAATGGCTCACTCTATTTTAAACAAGTATCAGAGTAATATCATCA
TCAAATACAGCTTTGATATGGGGAGAGTGCTTGCCCAACGAAGCCTGGAGTATGCTGGTTTTTC
ATAATGTTTACCCCTACACATGGGGTGGATTCTCTGACATCGACCTAATGGCTGATGAAATCG
GGCTGTGGGCTGTGTATGCAACTAACCAGAATGCAGGCAATATTGTCTCAGCCAACTTAACC
AAGATACCTTGGAGGTGATGAAGAGCTGGAGCACTGGCTACCCCAAGAGAAGTGCAGGGGAAT
CTTTCATGATCTGTGGGACACTGTATGTCACCAACTCCCCTTAACCTGGAGCCAAGGTGTATT
ATTCCTATTCCACCAAACCTCCACATATGAGTACACAGACATTCCTTCCATAACCAATACT
TTCACATATCCATGCTTGACTACAATGCAAGAGATCGAGCTCTCTATGCCTGGAACAATGGCC
ACCAGGTGCTGTTCAATGTCACCCTTTTCCATATCATCAAGACAGAGGATGACACAT**AG**GCAA
ATGTGACATGTTTTTCATTGATTTAAACAGTGTGATTTGTGATAAACTCTATAAGACCCCTTCC
GTTTTTTTCTTCACTATTATTTTTTCATCATTTCTCCAAAGCAAAGCATTTTTTATTGTAAAGTT
GGTGTTTCAAAAACATAGCTGAGCTTGTCTAACTTACCATGTTGGAAACACATCTTAACCTTCT
AAATTTACAAGGCCTATCATGTCTTGTGATGAAAAGCACTAAAAAAAAAAAAAGAGTTTAAAGT
GGCTAAAGTCATAGTTTTTGCAAGAGATTAATGATCTGCCTTATATTAGAGTCAGAGACTAATG
GTGGCTTAAATGCACGAATGTCTTTTTTTTTTAAAACTGTCATTTTTTTACTGTCTTTTGCTCCA
TCTCAGGAAATATTTTGGTAGGAATTAGGAGAACAAAAGCACTTTTATCCCATTTATTTCTT
TAAAAAATGTAAGGATTTCAATTTATATTGAAAAATAATATTAATCATTTTGTCTGTTAACACAA
TTCTCTGATGCGGTGCTGTACAGTCATTTTAAATCTCTTGCTAACATTTTATTGGCAGTATG
TATTTCTACCATTTGAACCACCATTTGTGCTATTGTATCTCTTCACTTCTGTGAAAGTAATATT
TTTTATAAANACACTGNAATTTTAAAAAAAAAAAAAAAAACAAAAAAAAAAAAAAAAAAAAA